



well-known in the art. The transgenic non-human animal can be from any species, including avians and non-human mammals. According to this aspect of the invention, suitable non-human mammals include mice, rats, rabbits, guinea pigs, goats, sheep, pigs and cattle. Suitable avians include chickens, ducks, geese, quail, turkeys and pheasants.

The nucleic acid encoding the CATERPILLER polypeptide or functional fragment can be stably incorporated into cells within the transgenic animal (typically, by stable integration into the genome or by stably maintained episomal constructs). It is not necessary that every cell contain the transgene, and the animal can be a chimera of modified and unmodified cells, as long as a sufficient number of cells comprise and express the nucleic acid encoding the CATERPILLER polypeptide or functional fragment so that the animal is a useful screening tool.

Exemplary methods of using the transgenic non-human animals of the invention for *in vivo* screening of compounds that modulate inflammatory response (both pro- and anti-inflammatory responses), cell survival (both pro- and anti-survival) and/or the activity of a CATERPILLER polypeptide comprise administering a test compound to a transgenic non-human animal (e.g., a mammal such as a mouse) comprising an isolated nucleic acid encoding a CATERPILLER polypeptide or functional fragment thereof stably incorporated into the genome, administering a test compound to the transgenic non-human animal, and detecting whether the test compound modulates inflammatory response, cell survival and/or CATERPILLER polypeptide activity (or the activity of a functional fragment). Other illustrative methods of the invention can be carried out to identify compounds that modulate MHC-II pathway activity, Toll-like receptor pathway activity, or NF- κ B activity *in vivo*.

It is known in the art how to measure these responses *in vivo*. Illustrative approaches include observation of changes that can be studied by gross examination (edema, redness, swelling, fever, tenderness), histopathology (cellular infiltrates, cell activation markers, phagocytosis, dead cells), changes in cytokine profiles, and cell surface markers (e.g., changes in TNF α , myeloperoxidase or CD69).

PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Books

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Range: from to ☐ Reverse complemented strand Features: ☐ SNP ☐ CDD ☒

1: AF389420. Reports Homo sapiens NOD2...[gi:28866920] [Links](#)

LOCUS AF389420 5601 bp mRNA linear PRI 06-MAR-2003

DEFINITION Homo sapiens NOD27 (NOD27) mRNA, complete cds.

ACCESSION AF389420

VERSION AF389420.1 GI:28866920

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1 (bases 1 to 5601)

AUTHORS Dowds, T.A., Masumoto, J., Chen, F.F., Ogura, Y., Inohara, N. and Nunez, G.

TITLE Regulation of cryopyrin/Pypaf1 signaling by pyrin, the familial Mediterranean fever gene product

JOURNAL Biochem. Biophys. Res. Commun. 302 (3), 575-580 (2003)

PUBMED 12615073

REFERENCE 2 (bases 1 to 5601)

AUTHORS Inohara, N.

TITLE Direct Submission

JOURNAL Submitted (04-JUN-2001) CCGC, University of Michigan, 1500 E.

Medical Center Dr., Ann Arbor, MI 48109, USA

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Range: from to ☐ Reverse complemented strand Features: ☐ SNP ☐ CDD ☒

1: AF526389. Reports *Homo sapiens* cryo...[gi:24461921]

Links

LOCUS AF526389 761 bp DNA linear PRI 14-JAN-2003

DEFINITION Homo sapiens cryopyrin (CIAS1) gene, intron 6.

ACCESSION AF526389

VERSION AF526389.1 GI:24461921

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1 (bases 1 to 761)

AUTHORS Hoffman, H.M., Mueller, J.L., Broide, D.H., Wanderer, A.A. and Kolodner, R.D.

TITLE Mutation of a new gene encoding a putative pyrin-like protein causes familial cold autoinflammatory syndrome and Muckle-Wells syndrome

JOURNAL Nat. Genet. 29 (3), 301-305 (2001)

PUBMED 11687797

REFERENCE 2 (bases 1 to 761)

AUTHORS Hoffman, H.M., Gregory, S.G., Mueller, J.L., Tresieras, M.,
Broide, D.H., Wanderer, A.A. and Kolodner, R.D.

TITLE Fine structure mapping of CIAS1: identification of an ancestral haplotype and a common FCAS mutation, L353P

JOURNAL Hum. Genet. 112 (2), 209-216 (2003)

PUBMED 12522564

REFERENCE 3 (bases 1 to 761)

AUTHORS Hoffman, H.M. and Mueller, J.L.

TITLE Direct Submission

JOURNAL Submitted (02-JUL-2002) Medicine, UCSD, 9500 Gilman Drive, La Jolla, CA 92093, USA

FEATURES	Location/Qualifiers
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Range: from to ☐ Reverse complemented strand Features: ☐ SNP ☐ CDD ☒

☐ 1: [AK025131](#). Reports Homo sapiens cDNA...[gi:10437587]

[Links](#)

LOCUS AK025131 2404 bp mRNA linear PRI 13-SEP-2003
DEFINITION Homo sapiens cDNA: FLJ21478 fis, clone COL05012.
ACCESSION AK025131
VERSION AK025131.1 GI:10437587
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Kawabata,A., Hikiji,T., Kobatake,N., Inagaki,H., Ikema,Y.,
Okamoto,S., Okitani,R., Ota,T., Suzuki,Y., Obayashi,M., Nishi,T.,
Shibahara,T., Tanaka,T., Nakamura,Y., Isogai,T. and Sugano,S.
TITLE NEDO human cDNA sequencing project
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2404)
AUTHORS Sugano,S., Suzuki,Y., Ota,T., Obayashi,M., Nishi,T., Isogai,T.,
Shibahara,T., Tanaka,T. and Nakamura,Y.
TITLE Direct Submission
JOURNAL Submitted (29-AUG-2000) Sumio Sugano, Institute of Medical Science,
University of Tokyo, Laboratory of Genome Structure Analysis, Human
Genome Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639,
Japan (E-mail:flcdna@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
Fax:81-3-5449-5416)
COMMENT NEDO human cDNA sequencing project supported by Ministry of
International Trade and Industry of Japan; cDNA full insert
sequencing: Research Association for Biotechnology; cDNA library
construction, 5'- & 3'-end one pass sequencing: Department of
Virology and Human Genome Center, Institute of Medical Science,
University of Tokyo (partly supported by Science and Technology
Agency).
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Range: from to ☐ Reverse complemented strand Features: ☐ SNP ☐ CDD ☒

1: [AK025212](#). Reports Homo sapiens cDNA...[gi:10437679] [Links](#)

LOCUS	AK025212	1912 bp	mRNA	linear	PRI 13-SEP-2003
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DEFINITION Homo sapiens cDNA: FLJ21559 fis, clone COL06406.

ACCESSION AK025212

VERSION AK025212.1 GI:10437679

KEYWORDS oligo capping; fis (full insert sequence).

SOURCE Homo sapiens (human)

ORGANISM	Homo sapiens
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1

AUTHORS Kawabata, A., Hikiji, T., Kobatake, N., Inagaki, H., Ikema, Y.,
Okamoto, S., Okitani, R., Ota, T., Suzuki, Y., Obayashi, M., Nishi, T.,
Shibahara, T., Tanaka, T., Nakamura, Y., Isoqai, T. and Sugano, S.

TITLE NEDO human cDNA sequencing project

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 1912)

AUTHORS Sugano, S., Suzuki, Y., Ota, T., Obayashi, M., Nishi, T., Isogai, T.,
Shibahara, T., Tanaka, T. and Nakamura, Y.

TITLE Direct Submission

JOURNAL Submitted (29-AUG-2000) Sumio Sugano, Institute of Medical Science,
University of Tokyo, Laboratory of Genome Structure Analysis, Human
Genome Center, Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639,
Japan (E-mail:flcdna@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
Fax:81-3-5449-5416)

COMMENT NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing: Department of Virology and Human Genome Center, Institute of Medical Science, University of Tokyo (partly supported by Science and Technology Agency).

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Range: from to ☐ Reverse complemented strand Features: ☐ SNP ☐ CDD ☒

☐ 1: [AK025362](#). Reports Homo sapiens cDNA...[gi:10437863]

[Links](#)

LOCUS AK025362 3495 bp mRNA linear PRI 13-SEP-2003

DEFINITION Homo sapiens cDNA: FLJ21709 fis, clone COL10077.

ACCESSION AK025362

VERSION AK025362.1 GI:10437863

KEYWORDS oligo capping; fis (full insert sequence).

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Kawabata,A., Hikiji,T., Kobatake,N., Inagaki,H., Ikema,Y., Okamoto,S., Okitani,R., Ota,T., Suzuki,Y., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T., Nakamura,Y., Isogai,T. and Sugano,S.

TITLE NEDO human cDNA sequencing project

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 3495)

AUTHORS Sugano,S., Suzuki,Y., Ota,T., Obayashi,M., Nishi,T., Isogai,T., Shibahara,T., Tanaka,T. and Nakamura,Y.

TITLE Direct Submission

JOURNAL Submitted (29-AUG-2000) Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure Analysis, Human Genome Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:flcdna@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286, Fax:81-3-5449-5416)

COMMENT NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing: Department of Virology and Human Genome Center, Institute of Medical Science, University of Tokyo (partly supported by Science and Technology Agency).

FEATURES

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Range: from to ☐ Reverse complemented strand Features: ☐ SNP ☐ CDD ☒

☐ 1: AK027416. Reports Homo sapiens cDNA...[gi:14042077]

Links

LOCUS AK027416 3308 bp mRNA linear PRI 30-JAN-2004

DEFINITION Homo sapiens cDNA FLJ14510 fis, clone NT2RM1000623, weakly similar to RIBONUCLEASE INHIBITOR.

ACCESSION AK027416

VERSION AK027416.1 GI:14042077

KEYWORDS oligo capping; fis (full insert sequence).

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE

AUTHORS

Ota,T., Suzuki,Y., Nishikawa,T., Otsuki,T., Sugiyama,T., Irie,R., Wakamatsu,A., Hayashi,K., Sato,H., Nagai,K., Kimura,K., Makita,H., Sekine,M., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T., Ishii,S., Yamamoto,J., Saito,K., Kawai,Y., Isono,Y., Nakamura,Y., Nagahari,K., Murakami,K., Yasuda,T., Iwayanagi,T., Wagatsuma,M., Shiratori,A., Sudo,H., Hosoiri,T., Kaku,Y., Kodaira,H., Kondo,H., Sugawara,M., Takahashi,M., Kanda,K., Yokoi,T., Furuya,T., Kikkawa,E., Omura,Y., Abe,K., Kamihara,K., Katsuta,N., Sato,K., Tanikawa,M., Yamazaki,M., Ninomiya,K., Ishibashi,T., Yamashita,H., Murakawa,K., Fujimori,K., Tanai,H., Kimata,M., Watanabe,M., Hiraoka,S., Chiba,Y., Ishida,S., Ono,Y., Takiguchi,S., Watanabe,S., Yosida,M., Hotuta,T., Kusano,J., Kanehori,K., Takahashi-Fujii,A., Hara,H., Tanase,T., Nomura,Y., Togiya,S., Komai,F., Hara,R., Takeuchi,K., Arita,M., Imose,N., Musashino,K., Yuuki,H., Oshima,A., Sasaki,N., Aotsuka,S., Yoshikawa,Y., Matsunawa,H., Ichihara,T., Shiohata,N., Sano,S., Moriya,S., Momiyama,H., Satoh,N., Takami,S., Terashima,Y., Suzuki,O., Nakagawa,S., Senoh,A., Mizoguchi,H., Goto,Y., Shimizu,F., Wakebe,H., Hishigaki,H., Watanabe,T., Sugiyama,A., Takemoto,M., Kawakami,B., Yamazaki,M., Watanabe,K., Kumagai,A., Itakura,S., Fukuzumi,Y., Fujimori,Y., Komiyama,M., Tashiro,H., Tanigami,A., Fujiwara,T., Ono,T., Yamada,K., Fujii,Y., Ozaki,K., Hirao,M., Ohmori,Y., Kawabata,A., Hikiji,T., Kobatake,N., Inagaki,H., Ikema,Y., Okamoto,S., Okitani,R., Kawakami,T., Noguchi,S., Itoh,T., Shigeta,K., Senba,T., Matsumura,K., Nakajima,Y., Mizuno,T., Morinaga,M., Sasaki,M., Togashi,T., Oyama,M., Hata,H., Watanabe,M., Komatsu,T., Mizushima-Sugano,J., Satoh,T., Shirai,Y., Takahashi,Y., Nakagawa,K., Okumura,K., Nagase,T., Nomura,N., Kikuchi,H., Masuho,Y., Yamashita,R., Nakai,K., Yada,T., Nakamura,Y., Ohara,O., Isoqai,T. and Sugano,S.

TITLE	Complete sequencing and characterization of 21,243 full-length human cDNAs
-------	--

JOURNAL Nat. Genet. 36 (1), 40-45 (2004)

PUBMED 14702039

REFERENCE 2
 AUTHORS Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y.,
 Nishikawa,T., Nagai,K., Sugano,S., Shiratori,A., Sudo,H.,
 Wagatsuma,M., Hosoiri,T., Kaku,Y., Kodaira,H., Kondo,H.,
 Sugawara,M., Takahashi,M., Chiba,Y., Ishida,S., Murakawa,K.,
 Ono,Y., Takiguchi,S., Watanabe,S., Kimura,K., Murakami,K.,
 Ishii,S., Kawai,Y., Saito,K., Yamamoto,J., Wakamatsu,A.,
 Nakamura,Y., Nagahari,K., Masuho,Y., Ninomiya,K. and Iwayanagi,T.

TITLE NEDO human cDNA sequencing project
 JOURNAL Unpublished

REFERENCE 3 (bases 1 to 3308)
 AUTHORS Isogai,T. and Otsuki,T.
 TITLE Direct Submission
 JOURNAL Submitted (10-MAY-2001) Takao Isogai, Helix Research Institute,
 Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
 (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

COMMENT NEDO human cDNA sequencing project supported by Ministry of
 Economy, Trade and Industry of Japan; cDNA full insert sequencing:
 Research Association for Biotechnology; cDNA library construction,
 5'- & 3'-end one pass sequencing and clone selection: Helix
 Research Institute (supported by Japan Key Technology Center etc.)
 and Department of Virology, Institute of Medical Science,
 University of Tokyo.

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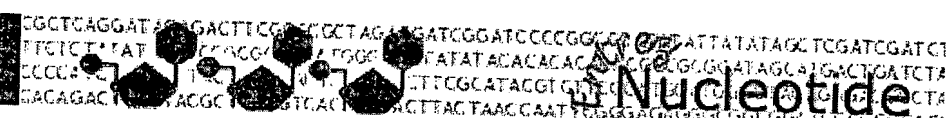
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Range: from to ☐ Reverse complemented strand

Features: ☐ SNP ☐ CDD ☒

☐ 1: [AK074109](#). Reports Homo sapiens mRNA...[gi:18676565]

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 Hominidae; Homo.

REFERENCE 1
 AUTHORS Jikuya,H., Takano,J., Nomura,N., Kikuno,R., Nagase,T. and Ohara,O.
 TITLE The nucleotide sequence of a long cDNA clone isolated from human spleen
 JOURNAL Published Only in Database (2002)

REFERENCE 2 (bases 1 to 4287)
 AUTHORS Jikuya,H., Takano,J., Nomura,N., Kikuno,R., Nagase,T. and Ohara,O.
 TITLE Direct Submission
 JOURNAL Submitted (21-JAN-2002) Takahiro Nagase, Kazusa DNA Research Institute, Department of Human Gene Research; 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp, URL:http://www.kazusa.or.jp/NEDO, Tel:81-438-52-3913, Fax:81-438-52-3914)

COMMENT NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert and 5'- & 3'-end one pass sequencing: Research Association for Biotechnology; cDNA library construction and clone selection: Kazusa DNA Research Institute.

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LOCUS AK074133 4121 bp mRNA linear PRI 15-FEB-2002

DEFINITION Homo sapiens mRNA for FLJ00206 protein.

ACCESSION AK074133

VERSION AK074133.1 GI:18676613

KEYWORDS fis (full insert sequence).

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1

AUTHORS Jikuya,H., Takano,J., Nomura,N., Kikuno,R., Nagase,T. and Ohara,O.

TITLE The nucleotide sequence of a long cDNA clone isolated from human spleen

JOURNAL Published Only in Database (2002)

REFERENCE 2 (bases 1 to 4121)

AUTHORS Jikuya,H., Takano,J., Nomura,N., Kikuno,R., Nagase,T. and Ohara,O.

TITLE Direct Submission

JOURNAL Submitted (21-JAN-2002) Takahiro Nagase, Kazusa DNA Research
Institute, Department of Human Gene Research; 1532-3, Yana,
Kisarazu, Chiba 292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp,
URL:http://www.kazusa.or.jp/NEDO, Tel:81-438-52-3913,
Fax:81-438-52-3914)

COMMENT NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert and 5'- &
3'-end one pass sequencing: Research Association for Biotechnology;
cDNA library construction and clone selection: Kazusa DNA Research
Institute.

FEATURES Location/Qualifiers

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/clone="FLJ00206"
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/inference="non-experimental evidence, no additional
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/note="Start codon is not identified."
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ORIGIN




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PubMed	Nucleotide	Protein	Genome	Structure	PMC	Taxonomy	OMIM	Books
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Limits Preview/Index History Clipboard Details

Display **GenBank**  Show **5**  Send to 

Range: from to ☐ Reverse complemented strand Features: ☐ SNP ☐ CDD ☒

1: AK074182. Reports Homo sapiens mRNA...[gi:18676711]

Links

LOCUS AK074182 4520 bp mRNA linear PRI 15-FEB-2002

DEFINITION Homo sapiens mRNA for FLJ00255 protein.

ACCESSION AK074182

VERSION AK074182.1 GI:18676711

KEYWORDS fis (full insert sequence).

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1

AUTHORS Jikuya, H., Takano, J., Nomura, N., Kikuno, R., Nagase, T. and Ohara, O.

TITLE The nucleotide sequence of a long cDNA clone isolated from human spleen

JOURNAL Published Only in Database (2002)

REFERENCE 2 (bases 1 to 4520)

AUTHORS Jikuya, H., Takano, J., Nomura, N., Kikuno, R., Nagase, T. and Ohara, O.

TITLE Direct Submission

JOURNAL Submitted (21-JAN-2002) Takahiro Nagase, Kazusa DNA Research Institute, Department of Human Gene Research; 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp, URL:<http://www.kazusa.or.jp/NEDO>, Tel:81-438-52-3913, Fax:81-438-52-3914)

COMMENT NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert and 5'- & 3'-end one pass sequencing: Research Association for Biotechnology; cDNA library construction and clone selection: Kazusa DNA Research Institute.

FEATURES

Location/Qualifiers

source

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ORIGIN

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CCCATCT

SACAGACT

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☐ 1: [AK090431](#). Reports Homo sapiens mRNA...[gi:21748549]

[Links](#)

LOCUS AK090431 6604 bp mRNA linear PRI 15-JUL-2002

DEFINITION Homo sapiens mRNA for FLJ00348 protein.

ACCESSION AK090431

VERSION AK090431.1 GI:21748549

KEYWORDS fis (full insert sequence).

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1

AUTHORS Jikuya,H., Takano,J., Kikuno,R., Nagase,T. and Ohara,O.

TITLE The nucleotide sequence of a long cDNA clone isolated from human spleen

JOURNAL Published Only in Database (2002)

REFERENCE 2 (bases 1 to 6604)

AUTHORS Jikuya,H., Takano,J., Kikuno,R., Nagase,T. and Ohara,O.

TITLE Direct Submission

JOURNAL Submitted (04-JUL-2002) Takahiro Nagase, Kazusa DNA Research Institute, Department of Human Gene Research; 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp, URL:http://www.kazusa.or.jp/NEDO, Tel:81-438-52-3913, Fax:81-438-52-3914)

COMMENT NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert and 5'- & 3'-end one pass sequencing: Research Association for Biotechnology; cDNA library construction and clone selection: Kazusa DNA Research Institute.

FEATURES Location/Qualifiers

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Oct 4 2005 13:52:42



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PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Books

Search for Display Range: from to ☐ Reverse complemented strand Features: ☐ SNP ☐ CDD ☒☐ 1: [AK090439](#). Reports Homo sapiens mRNA...[gi:21748565][Links](#)

LOCUS AK090439 5833 bp mRNA linear PRI 15-JUL-2002

DEFINITION Homo sapiens mRNA for FLJ00359 protein.

ACCESSION AK090439

VERSION AK090439.1 GI:21748565

KEYWORDS fis (full insert sequence).

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1

AUTHORS Jikuya,H., Takano,J., Kikuno,R., Nagase,T. and Ohara,O.

TITLE The nucleotide sequence of a long cDNA clone isolated from human spleen

JOURNAL Published Only in Database (2002)

REFERENCE 2 (bases 1 to 5833)

AUTHORS Jikuya,H., Takano,J., Kikuno,R., Nagase,T. and Ohara,O.

TITLE Direct Submission

JOURNAL Submitted (04-JUL-2002) Takahiro Nagase, Kazusa DNA Research Institute, Department of Human Gene Research; 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp, URL:http://www.kazusa.or.jp/NEDO, Tel:81-438-52-3913, Fax:81-438-52-3914)

COMMENT NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert and 5'- & 3'-end one pass sequencing; Research Association for Biotechnology; cDNA library construction and clone selection: Kazusa DNA Research Institute.

FEATURES

Location/Qualifiers

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Oct 4 2005 13:52:42




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PubMed	Nucleotide	Protein	Genome	Structure	PMC	Taxonomy	OMIM	Books
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Range: from to ☐ Reverse complemented strand Features: ☐ SNP ☐ CDD ☒

1: [AK090476](#). Reports Homo sapiens mRNA...[gi:21748639]

Links

LOCUS AK090476 4191 bp mRNA linear PRI 15-JUL-2002

DEFINITION Homo sapiens mRNA for FLJ00398 protein.

ACCESSION AK090476

VERSION AK090476.1 GI:21748639

KEYWORDS `fis` (full insert sequence).

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1

AUTHORS Jikuya, H., Takano, J., Kikuno, R., Nagase, T. and Ohara, O.

TITLE The nucleotide sequence of a long cDNA clone isolated from human spleen

JOURNAL Published Only in Database (2002)

REFERENCE 2 (bases 1 to 4191)

AUTHORS Jikuya, H., Takano, J., Kikuno, R., Nagase, T. and Ohara, O.

TITLE Direct Submission

JOURNAL Submitted (04-JUL-2002) Takahiro Nagase, Kazusa DNA Research Institute, Department of Human Gene Research; 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp, URL:<http://www.kazusa.or.jp/NEDO>, Tel:81-438-52-3913, Fax:81-438-52-3914)

COMMENT	NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert and 5'- & 3'-end one pass sequencing: Research Association for Biotechnology; cDNA library construction and clone selection: Kazusa DNA Research Institute.
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FEATURES	Location/Qualifiers
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ORIGIN

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Range: from to ☐ Reverse complemented strand Features: ☐ SNP ☐ CDD ☒

☐ 1: [AK097030](#). Reports Homo sapiens cDNA...[gi:21756666]

[Links](#)

LOCUS AK097030 2712 bp mRNA linear PRI 30-JAN-2004
DEFINITION Homo sapiens cDNA FLJ39711 fis, clone SMINT2013032.
ACCESSION AK097030
VERSION AK097030.1 GI:21756666
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Ota,T., Suzuki,Y., Nishikawa,T., Otsuki,T., Sugiyama,T., Irie,R.,
Wakamatsu,A., Hayashi,K., Sato,H., Nagai,K., Kimura,K., Makita,H.,
Sekine,M., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T.,
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Nagahari,K., Murakami,K., Yasuda,T., Iwayanagi,T., Wagatsuma,M.,
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Goto,Y., Shimizu,F., Wakebe,H., Hishigaki,H., Watanabe,T.,
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Satoh,T., Shirai,Y., Takahashi,Y., Nakagawa,K., Okumura,K.,
Nagase,T., Nomura,N., Kikuchi,H., Masuho,Y., Yamashita,R.,
Nakai,K., Yada,T., Nakamura,Y., Ohara,O., Isogai,T. and Sugano,S.
TITLE Complete sequencing and characterization of 21,243 full-length
human cDNAs
JOURNAL Nat. Genet. 36 (1), 40-45 (2004)
PUBMED [14702039](#)
REFERENCE 2

AUTHORS Tashiro,H., Yamazaki,M., Watanabe,K., Kumagai,A., Itakura,S.,
Fukuzumi,Y., Fujimori,Y., Komiyama,M., Sugiyama,T., Irie,R.,
Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S., Yamamoto,J., Isono,Y.,
Kawai-Hio,Y., Saito,K., Nishikawa,T., Kimura,K., Yamashita,H.,
Matsuo,K., Nakamura,Y., Sekine,M., Kikuchi,H., Kanda,K.,
Wagatsuma,M., Murakawa,K., Kanehori,K., Takahashi-Fujii,A.,
Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S.,
Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T.

TITLE NEDO human cDNA sequencing project

JOURNAL Unpublished

REFERENCE 3 (bases 1 to 2712)

AUTHORS Isogai,T. and Yamamoto,J.

TITLE Direct Submission

JOURNAL Submitted (04-JUL-2002) Takao Isogai, FLJ Project(HRI Team); 2-6-7
Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

COMMENT NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library
construction: Helix Research Institute (HRI) (supported by Japan
Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
HRI, and Biotechnology Center, National Institute of Technology and
Evaluation; clone selection for full insert sequencing: HRI and
RAB; annotation: HRI and RAB.

FEATURES Location/Qualifiers

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ORIGIN

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Range: from to ☐ Reverse complemented strand Features: ☐ SNP ☐ CDD ☒

☐ 1: AY051112. Reports Homo sapiens cryo...[gi:17027229]

[Links](#)

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DEFINITION Homo sapiens cryopyrin (CIAS1) gene, exon 1.
ACCESSION AY051112
VERSION AY051112.1 GI:17027229
KEYWORDS .
SEGMENT 1 of 8
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 1146)
AUTHORS Hoffman,H.M., Mueller,J.L., Broide,D.H., Wanderer,A.A. and
Kolodner,R.D.
TITLE Mutation of a new gene encoding a putative pyrin-like protein
causes familial cold autoinflammatory syndrome and Muckle-Wells
syndrome
JOURNAL Nat. Genet. 29 (3), 301-305 (2001)
PUBMED [11687797](#)
REFERENCE 2 (bases 1 to 1146)
AUTHORS Hoffman,H.M., Mueller,J.L. and Kolodner,R.D.
TITLE Direct Submission
JOURNAL Submitted (15-AUG-2001) Medicine, UCSD, 9500 Gilman Drive, La
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Range: from to ☐ Reverse complemented strand Features: ☐ SNP ☐ CDD ☒

□1: [AY051113](#). Reports *Homo sapiens* cryo...[gi:17027230]

Links

LOCUS	AY051112S2	473 bp	DNA	linear	PRI 21-NOV-2001
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DEFINITION Homo sapiens cryopyrin (CIAS1) gene, exon 2.

ACCESSION AY051113

VERSION AY051113.1 GI:17027230

KEYWORDS

SEGMENT 2 of 8

SOURCE	Homo sapiens (human)
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ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1 (bases 1 to 473)

AUTHORS Hoffman, H.M., Mueller, J.L., Broide, D.H., Wanderer, A.A. and Kolodner, R.D.

TITLE Mutation of a new gene encoding a putative pyrin-like protein causes familial cold autoinflammatory syndrome and Muckle-Wells syndrome

JOURNAL Nat. Genet. 29 (3), 301-305 (2001)

PUBMED 11687797

REFERENCE 2 (bases 1 to 473)

AUTHORS Hoffman, H.M., Mueller, J.L. and Kolodner, R.D.

TITLE Direct Submission

JOURNAL Submitted (15-AUG-2001) Medicine, UCSD, 9500 Gilman Drive, La Jolla, CA 92093-0635, USA

FEATURES	Location/Qualifiers
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☐ 1: [AY051114](#). Reports [Homo sapiens cryo...](#)[gi:17027231]

[Links](#)

LOCUS AY051112S3 1958 bp DNA linear PRI 21-NOV-2001

DEFINITION [Homo sapiens cryopyrin \(CIAS1\) gene, exon 3.](#)

ACCESSION [AY051114](#)

VERSION [AY051114.1](#) [GI:17027231](#)

KEYWORDS

SEGMENT 3 of 8

SOURCE [Homo sapiens \(human\)](#)

ORGANISM [Homo sapiens](#)

[Eukaryota](#); [Metazoa](#); [Chordata](#); [Craniata](#); [Vertebrata](#); [Euteleostomi](#);
[Mammalia](#); [Eutheria](#); [Euarchontoglires](#); [Primates](#); [Catarrhini](#);
[Hominidae](#); [Homo](#).

REFERENCE 1 (bases 1 to 1958)

AUTHORS Hoffman,H.M., Mueller,J.L., Broide,D.H., Wanderer,A.A. and
 Kolodner,R.D.

TITLE Mutation of a new gene encoding a putative pyrin-like protein
 causes familial cold autoinflammatory syndrome and Muckle-Wells
 syndrome

JOURNAL [Nat. Genet.](#) 29 (3), 301-305 (2001)

PUBMED [11687797](#)

REFERENCE 2 (bases 1 to 1958)

AUTHORS Hoffman,H.M., Mueller,J.L. and Kolodner,R.D.

TITLE Direct Submission

JOURNAL Submitted (15-AUG-2001) Medicine, UCSD, 9500 Gilman Drive, La
 Jolla, CA 92093-0635, USA

FEATURES Location/Qualifiers

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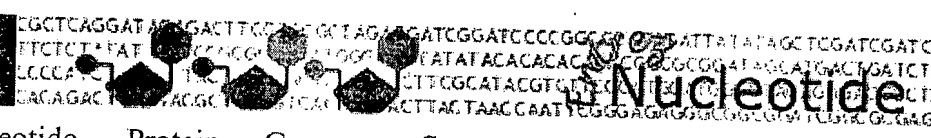
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Range: from to ☐ Reverse complemented strand Features: ☐ SNP ☐ CDD ☒

☐ 1: [AY051115](#). Reports Homo sapiens cryo...[gi:17027233]

[Links](#)

LOCUS AY051112S5 325 bp DNA linear PRI 21-NOV-2001
 DEFINITION Homo sapiens cryopyrin (CIAS1) gene, exon 5.
 ACCESSION AY051115
 VERSION AY051115.1 GI:17027233
 KEYWORDS .
 SEGMENT 5 of 8
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 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.
 REFERENCE 1 (bases 1 to 325)
 AUTHORS Hoffman,H.M., Mueller,J.L., Broide,D.H., Wanderer,A.A. and
 Kolodner,R.D.
 TITLE Mutation of a new gene encoding a putative pyrin-like protein
 causes familial cold autoinflammatory syndrome and Muckle-Wells
 syndrome
 JOURNAL Nat. Genet. 29 (3), 301-305 (2001)
 PUBMED [11687797](#)
 REFERENCE 2 (bases 1 to 325)
 AUTHORS Hoffman,H.M., Mueller,J.L. and Kolodner,R.D.
 TITLE Direct Submission
 JOURNAL Submitted (15-AUG-2001) Medicine, UCSD, 9500 Gilman Drive, La
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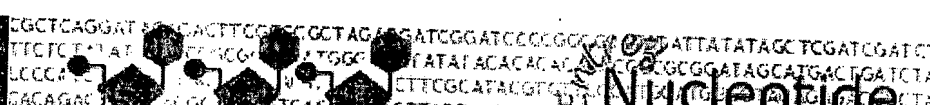
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Range: from to ☐ Reverse complemented strand

Features:

☐ SNP☐ CDD☒

☐ 1: [AY051116](#). Reports *Homo sapiens cryo...*[gi:17027235]

Links

LOCUS AY051112S7 1305 bp DNA linear PRI 21-NOV-2001
DEFINITION *Homo sapiens cryopyrin (CIAS1) gene, exons 7 and 8.*
ACCESSION AY051116
VERSION AY051116.1 GI:17027235
KEYWORDS .
SEGMENT 7 of 8
SOURCE *Homo sapiens* (human)
ORGANISM *Homo sapiens*
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1305)
AUTHORS Hoffman,H.M., Mueller,J.L., Broide,D.H., Wanderer,A.A. and Kolodner,R.D.
TITLE Mutation of a new gene encoding a putative pyrin-like protein causes familial cold autoinflammatory syndrome and Muckle-Wells syndrome
JOURNAL Nat. Genet. 29 (3), 301-305 (2001)
PUBMED 11687797
REFERENCE 2 (bases 1 to 1305)
AUTHORS Hoffman,H.M., Mueller,J.L. and Kolodner,R.D.
TITLE Direct Submission
JOURNAL Submitted (15-AUG-2001) Medicine, UCSD, 9500 Gilman Drive, La Jolla, CA 92093-0635, USA
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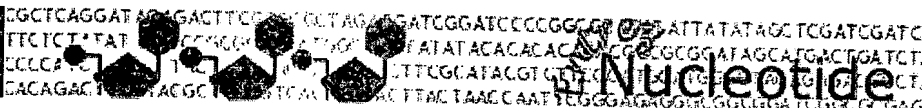
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Display ☒ Show ☒ Send to ☒

Range: from to ☐ Reverse complemented strand Features: ☐ SNP ☐ CDD ☒

☐ 1: [AY051117](#). Reports Homo sapiens cryo...[gi:17027236]

[Links](#)

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 DEFINITION Homo sapiens cryopyrin (CIAS1) gene, exon 9 and complete cds, alternatively spliced.
 ACCESSION AY051117
 VERSION AY051117.1 GI:17027236
 KEYWORDS .
 SEGMENT 8 of 8
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 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 480)
 AUTHORS Hoffman,H.M., Mueller,J.L., Broide,D.H., Wanderer,A.A. and Kolodner,R.D.
 TITLE Mutation of a new gene encoding a putative pyrin-like protein causes familial cold autoinflammatory syndrome and Muckle-Wells syndrome
 JOURNAL Nat. Genet. 29 (3), 301-305 (2001)
 PUBMED 11687797
 REFERENCE 2 (bases 1 to 480)
 AUTHORS Hoffman,H.M., Mueller,J.L. and Kolodner,R.D.
 TITLE Direct Submission
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Range: from to ☐ Reverse complemented strand Features: ☐ SNP ☐ CDD ☒

☐ 1: [AY056059](#). Reports Homo sapiens cryo...[gi:17027232]

[Links](#)

LOCUS AY051112S4 385 bp DNA linear PRI 21-NOV-2001

DEFINITION Homo sapiens cryopyrin (CIAS1) gene, exon 4.

ACCESSION AY056059

VERSION AY056059.1 GI:17027232

KEYWORDS .

SEGMENT 4 of 8

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
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 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.

REFERENCE 1 (bases 1 to 385)

AUTHORS Hoffman,H.M., Mueller,J.L., Broide,D.H., Wanderer,A.A. and
 Kolodner,R.D.

TITLE Mutation of a new gene encoding a putative pyrin-like protein
 causes familial cold autoinflammatory syndrome and Muckle-Wells
 syndrome

JOURNAL Nat. Genet. 29 (3), 301-305 (2001)

PUBMED [11687797](#)

REFERENCE 2 (bases 1 to 385)

AUTHORS Hoffman,H.M., Mueller,J.L. and Kolodner,R.D.

TITLE Direct Submission

JOURNAL Submitted (15-AUG-2001) Medicine, UCSD, 9500 Gilman Drive, La
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Range: from to ☐ Reverse complemented strand Features: ☐ SNP ☐ CDD ☒

☐ 1: [AY056060](#). Reports Homo sapiens cryo...[gi:17027234]

[Links](#)

LOCUS AY051112S6 411 bp DNA linear PRI 21-NOV-2001
DEFINITION Homo sapiens cryopyrin (CIAS1) gene, exon 6.
ACCESSION AY056060
VERSION AY056060.1 GI:17027234
KEYWORDS .
SEGMENT 6 of 8
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 411)
AUTHORS Hoffman,H.M., Mueller,J.L., Broide,D.H., Wanderer,A.A. and
Kolodner,R.D.
TITLE Mutation of a new gene encoding a putative pyrin-like protein
causes familial cold autoinflammatory syndrome and Muckle-Wells
syndrome
JOURNAL Nat. Genet. 29 (3), 301-305 (2001)
PUBMED [11687797](#)
REFERENCE 2 (bases 1 to 411)
AUTHORS Hoffman,H.M., Mueller,J.L. and Kolodner,R.D.
TITLE Direct Submission
JOURNAL Submitted (15-AUG-2001) Medicine, UCSD, 9500 Gilman Drive, La
Jolla, CA 92093-0635, USA
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LOCUS AY092033 3237 bp mRNA linear PRI 22-APR-2002
DEFINITION *Homo sapiens* NALP3 intermediate isoform (NALP3) mRNA, complete cds.
ACCESSION AY092033
VERSION AY092033.1 GI:20268803
KEYWORDS .
SOURCE *Homo sapiens* (human)
ORGANISM *Homo sapiens*
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; *Homo*.
REFERENCE 1 (bases 1 to 3237)
AUTHORS Aganna, E., Martinon, F., Hawkins, P.N., Ross, J.B., Swan, D.C.,
Booth, D.R., Lachmann, H.J., Gaudet, R., Cotter, F.E., Thome, M.,
Hitmann, G.A., Tschopp, J. and McDermott, M.F.
TITLE Mutations in the NALP3 gene are associated with autoinflammatory
disorders distinguished by recurrent fever, cold sensitivity,
sensorineural deafness and frequent AA amyloidosis
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 3237)
AUTHORS Martinon, F. and Tschopp, J.
TITLE Direct Submission
JOURNAL Submitted (27-MAR-2002) Biochemistry, University of Lausanne, Ch.
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Display ☒ Show ☒ Send to ☒

Range: from to ☐ Reverse complemented strand Features: ☐ SNP ☐ CDD ☒

☐ 1: [AY116204](#). Reports *Homo sapiens mona...*[gi:21711820]

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LOCUS AY116204 3731 bp mRNA linear PRI 21-MAY-2003
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 VERSION AY116204.1 GI:21711820
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 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.
 REFERENCE 1 (bases 1 to 3731)
 AUTHORS Williams,K.L., Taxman,D.J., Linhoff,M.W., Reed,W. and Ting,J.P.Y.
 TITLE Monarch-1: A Pyrin/Nucleotide-Binding Domain/Leucine-Rich Repeat
 Protein That Controls Classical and Nonclassical MHC Class I Genes
 J. Immunol. 170 (11), 5354-5358 (2003)
 JOURNAL J. Immunol. 170 (11), 5354-5358 (2003)
 PUBMED 12759408
 REFERENCE 2 (bases 1 to 3731)
 AUTHORS Williams,K.L., Linhoff,M.W., Harton,J.A. and Ting,J.P.Y.
 TITLE Direct Submission
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Range: from to ☐ Reverse complemented strand Features: ☐ SNP ☐ CDD ☒

☐ 1: [AY116205](#). Reports *Homo sapiens mona...*[gi:21711822]

[Links](#)

LOCUS AY116205 3563 bp mRNA linear PRI 21-MAY-2003

DEFINITION *Homo sapiens monarch-1 splice form II mRNA, complete cds; alternatively spliced.*

ACCESSION AY116205

VERSION AY116205.1 GI:21711822

KEYWORDS .

SOURCE *Homo sapiens* (human)

ORGANISM *Homo sapiens*

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 3563)

AUTHORS Williams, K.L., Taxman, D.J., Linhoff, M.W., Reed, W. and Ting, J.P.Y.

TITLE Monarch-1: A Pyrin/Nucleotide-Binding Domain/Leucine-Rich Repeat Protein That Controls Classical and Nonclassical MHC Class I Genes

JOURNAL J. Immunol. 170 (11), 5354-5358 (2003)

PUBMED 12759408

REFERENCE 2 (bases 1 to 3563)

AUTHORS Williams, K.L., Linhoff, M.W. and Ting, J.P.Y.

TITLE Direct Submission

JOURNAL Submitted (29-MAY-2002) Lineberger Cancer Center, UNC, Mason Farm Road, Chapel Hill, NC 27599, USA

FEATURES Location/Qualifiers

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PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Books

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Range: from to ☐ Reverse complemented strand Features: ☐ SNP ☐ CDD ☒

☐ 1: [AY116206](#). Reports [Homo sapiens mona...\[gi:21711824\]](#)

[Links](#)

LOCUS AY116206 3395 bp mRNA linear PRI 21-MAY-2003

DEFINITION [Homo sapiens monarch-1 splice form III mRNA, complete cds; alternatively spliced.](#)

ACCESSION AY116206

VERSION AY116206.1 GI:21711824

KEYWORDS .

SOURCE [Homo sapiens \(human\)](#)

ORGANISM [Homo sapiens](#)

[Eukaryota](#); [Metazoa](#); [Chordata](#); [Craniata](#); [Vertebrata](#); [Euteleostomi](#); [Mammalia](#); [Eutheria](#); [Euarchontoglires](#); [Primates](#); [Catarrhini](#); [Hominidae](#); [Homo](#).

REFERENCE 1 (bases 1 to 3395)

AUTHORS Williams, K.L., Taxman, D.J., Linhoff, M.W., Reed, W. and Ting, J.P.Y.

TITLE Monarch-1: A Pyrin/Nucleotide-Binding Domain/Leucine-Rich Repeat Protein That Controls Classical and Nonclassical MHC Class I Genes

JOURNAL J. Immunol. 170 (11), 5354-5358 (2003)

PUBMED [12759408](#)

REFERENCE 2 (bases 1 to 3395)

AUTHORS Williams, K.L., Linhoff, M.W. and Ting, J.P.Y.

TITLE Direct Submission

JOURNAL Submitted (29-MAY-2002) Lineberger Cancer Center, UNC, Mason Farm Road, Chapel Hill, NC 27599, USA

FEATURES Location/Qualifiers

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Display ☒ Show ☒ Send to ☒Range: from to ☐ Reverse complemented strand Features: ☐ SNP ☐ CDD ☒☐ 1: [AY116207](#). Reports Homo sapiens mona...[gi:21711826][Links](#)

LOCUS AY116207 3221 bp mRNA linear PRI 21-MAY-2003

DEFINITION Homo sapiens monarch-1 splice form IV mRNA, complete cds;
alternatively spliced.

ACCESSION AY116207

VERSION AY116207.1 GI:21711826

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1 (bases 1 to 3221)

AUTHORS Williams, K.L., Taxman, D.J., Linhoff, M.W., Reed, W. and Ting, J.P.Y.

TITLE Monarch-1: A Pyrin/Nucleotide-Binding Domain/Leucine-Rich Repeat
Protein That Controls Classical and Nonclassical MHC Class I Genes

J. Immunol. 170 (11), 5354-5358 (2003)

PUBMED 12759408

REFERENCE 2 (bases 1 to 3221)

AUTHORS Williams, K.L., Linhoff, M.W. and Ting, J.P.Y.

TITLE Direct Submission

JOURNAL Submitted (29-MAY-2002) Lineberger Cancer Center, UNC, Mason Farm
Road, Chapel Hill, NC 27599, USA

FEATURES Location/Qualifiers

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Range: from to ☐ Reverse complemented strand Features: ☐ SNP ☐ CDD ☒

1: [AY154469](#). Reports Homo sapiens NALP...[gi:28436381] [Links](#)

LOCUS	AY154469	3282 bp	mRNA	linear	PRI 20-FEB-2003
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DEFINITION Homo sapiens NALP14 (NALP14) mRNA, complete cds.

ACCESSION AY154469

VERSION AY154469.1 GI:28436381

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1 (bases 1 to 3282)

AUTHORS Tschopp, J., Martinon, F. and Burns, K.

TITLE NALPs: a novel protein family involved in inflammation

JOURNAL Nat. Rev. Mol. Cell Biol. 4 (2), 95-104 (2003)

PUBMED 12563287

REFERENCE 2 (bases 1 to 3282)

AUTHORS Martinon, F., Hofmann, K. and Tschopp, J.

TITLE Direct Submission

JOURNAL Submitted (25-SEP-2002) Institute of Biochemistry, University of
Lausanne, ch. des Boveresses 155, Epalinges, VD 1066, Switzerland

FEATURES	Location/Qualifiers
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☐ 1: [BC013199](#). Reports Homo sapiens NOD9...[gi:16753263] [Links](#)

LOCUS	BC013199	2177 bp	mRNA	linear	PRI 27-APR-2005
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DEFINITION Homo sapiens NOD9 protein, mRNA (cDNA clone IMAGE:4387619), partial cds.

ACCESSION BC013199

VERSION BC013199.1 GI:16753263

KEYWORDS

SOURCE	Homo sapiens (human)
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ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1 (bases 1 to 2177)

AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H.; Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
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Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
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Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
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Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.

CONSRTM Mammalian Gene Collection Program Team

TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
-------	--

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
PUBMED 12477932

REFERENCE 2 (bases 1 to 2177)

AUTHORS
CONSRTM NIH MGC Project

TITLE Direct Submission

JOURNAL Submitted (27-AUG-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Bethesda, MD 20892-2590, USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>

COMMENT Contact: MGC help desk
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Baylor College of Medicine Human Genome
 Sequencing Center
 Center code: BCM-HGSC
 Web site: <http://www.hqsc.bcm.tmc.edu/cdna/>
 Contact: amg@bcm.tmc.edu

Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
 Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
 A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAK Plate: 26 Row: p Column: 19.

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PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Books

Search for Display 5 Range: from to ☐ Reverse complemented strand Features: ☐ SNP ☐ CDD ☒☐ 1: [NM_004895](#). Reports Homo sapiens cold...[gi:34878692][Links](#)

LOCUS NM_004895 4484 bp mRNA linear PRI 17-OCT-2005
DEFINITION Homo sapiens cold autoinflammatory syndrome 1 (CIAS1), transcript variant 1, mRNA.
ACCESSION NM_004895
VERSION NM_004895.3 GI:34878692
KEYWORDS .
SOURCE Homo sapiens (human)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 4484)
AUTHORS Arostegui,J.I., Aldea,A., Modesto,C., Rua,M.J., Arguelles,F., Gonzalez-Ensenat,M.A., Ramos,E., Rius,J., Plaza,S., Vives,J. and Yague,J.
TITLE Clinical and genetic heterogeneity among Spanish patients with recurrent autoinflammatory syndromes associated with the CIAS1/PYPAF1/NALP3 gene
JOURNAL Arthritis Rheum. 50 (12), 4045-4050 (2004)
PUBMED [15593220](#)
REMARK GeneRIF: Missense mutations of CIAS1/PYPAF1/NALP3 gene occurred in 7 unrelated Spanish families with recurrent autoinflammatory diseases.
REFERENCE 2 (bases 1 to 4484)
AUTHORS Dowds,T.A., Masumoto,J., Zhu,L., Inohara,N. and Nunez,G.
TITLE Cryopyrin-induced interleukin 1beta secretion in monocytic cells: enhanced activity of disease-associated mutants and requirement for ASC
JOURNAL J. Biol. Chem. 279 (21), 21924-21928 (2004)
PUBMED [15020601](#)
REMARK GeneRIF: cryopyrin disease-associated mutants are constitutively active and able to induce NF-kappaB activation and IL-1beta secretion at least in part by an increased ability to interact with ASC
REFERENCE 3 (bases 1 to 4484)
AUTHORS Neven,B., Callebaut,I., Prieur,A.M., Feldmann,J., Bodemer,C., Lepore,L., Derfalvi,B., Benjaponpitak,S., Vesely,R., Sauvain,M.J., Oertle,S., Allen,R., Morgan,G., Borkhardt,A., Hill,C., Gardner-Medwin,J., Fischer,A. and de Saint Basile,G.
TITLE Molecular basis of the spectral expression of CIAS1 mutations associated with phagocytic cell-mediated autoinflammatory disorders CINCA/NOMID, MWS, and FCU
JOURNAL Blood 103 (7), 2809-2815 (2004)
PUBMED [14630794](#)
REMARK GeneRIF: mutated in CINCA syndrome

- REFERENCE 4 (bases 1 to 4484)
AUTHORS Agostini,L., Martinon,F., Burns,K., McDermott,M.F., Hawkins,P.N. and Tschopp,J.
TITLE NALP3 forms an IL-1beta-processing inflammasome with increased activity in Muckle-Wells autoinflammatory disorder
JOURNAL Immunity 20 (3), 319-325 (2004)
PUBMED [15030775](#)
REMARK GeneRIF: NALP3 forms a protein complex that processes IL-1 beta in macrophages from a patient with the Muckle-Wells autoinflammatory disorder.
- REFERENCE 5 (bases 1 to 4484)
AUTHORS O'Connor,W. Jr., Harton,J.A., Zhu,X., Linhoff,M.W. and Ting,J.P.
TITLE Cutting edge: CIAS1/cryopyrin/PYPAF1/NALP3/CATERPILLER 1.1 is an inducible inflammatory mediator with NF-kappa B suppressive properties
JOURNAL J. Immunol. 171 (12), 6329-6333 (2003)
PUBMED [14662828](#)
REMARK GeneRIF: CIAS1/cryopyrin may act as a key regulator of inflammation, induced to dampen NF-kappa B-dependent proinflammatory signals.
- REFERENCE 6 (bases 1 to 4484)
AUTHORS Dowds,T.A., Masumoto,J., Chen,F.F., Ogura,Y., Inohara,N. and Nunez,G.
TITLE Regulation of cryopyrin/Pypaf1 signaling by pyrin, the familial Mediterranean fever gene product
JOURNAL Biochem. Biophys. Res. Commun. 302 (3), 575-580 (2003)
PUBMED [12615073](#)
REMARK GeneRIF: there is a cryopyrin signaling pathway activated through the induced proximity of ASC, which is negatively regulated by pyrin
- REFERENCE 7 (bases 1 to 4484)
AUTHORS Tschopp,J., Martinon,F. and Burns,K.
TITLE NALPs: a novel protein family involved in inflammation
JOURNAL Nat. Rev. Mol. Cell Biol. 4 (2), 95-104 (2003)
PUBMED [12563287](#)
REMARK Review article
- REFERENCE 8 (bases 1 to 4484)
AUTHORS Hoffman,H.M., Gregory,S.G., Mueller,J.L., Tresieras,M., Broide,D.H., Wanderer,A.A. and Kolodner,R.D.
TITLE Fine structure mapping of CIAS1: identification of an ancestral haplotype and a common FCAS mutation, L353P
JOURNAL Hum. Genet. 112 (2), 209-216 (2003)
PUBMED [12522564](#)
REMARK GeneRIF: a single heterozygous missense mutation (T1058C=L353P) in exon 3 of CIAS1 in all four families that is responsible for the large majority of FCAS cases
- REFERENCE 9 (bases 1 to 4484)
AUTHORS Granel,B., Philip,N., Serratrice,J., Ene,N., Grateau,G., Dode,C., Cuisset,L., Disdier,P., Berbis,P., Delpech,M. and Weiller,P.J.
TITLE CIAS1 mutation in a patient with overlap between Muckle-Wells and chronic infantile neurological cutaneous and articular syndromes
JOURNAL Dermatology (Basel) 206 (3), 257-259 (2003)
PUBMED [12673085](#)
- REFERENCE 10 (bases 1 to 4484)
AUTHORS Aksentijevich,I., Nowak,M., Mallah,M., Chae,J.J., Watford,W.T., Hofmann,S.R., Stein,L., Russo,R., Goldsmith,D., Dent,P., Rosenberg,H.F., Austin,F., Remmers,E.F., Balow,J.E. Jr., Rosenzweig,S., Komarow,H., Shoham,N.G., Wood,G., Jones,J., Mangra,N., Carrero,H., Adams,B.S., Moore,T.L., Schikler,K., Hoffman,H., Lovell,D.J., Lipnick,R., Barron,K., O'Shea,J.J.,

TITLE Kastner,D.L. and Goldbach-Mansky,R.
 De novo CIAS1 mutations, cytokine activation, and evidence for genetic heterogeneity in patients with neonatal-onset multisystem inflammatory disease (NOMID): a new member of the expanding family of pyrin-associated autoinflammatory diseases
 JOURNAL Arthritis Rheum. 46 (12), 3340-3348 (2002)
 PUBMED [12483741](#)
 REMARK GeneRIF: De novo CIAS1 mutations in neonatal-onset multisystem inflammatory disease. We found 6 heterozygous missense substitutions in CIAS1. Germline mutations.
 REFERENCE 11 (bases 1 to 4484)
 AUTHORS Fiorentino,L., Stehlik,C., Oliveira,V., Ariza,M.E., Godzik,A. and Reed,J.C.
 TITLE A novel PAAD-containing protein that modulates NF-kappa B induction by cytokines tumor necrosis factor-alpha and interleukin-1beta
 JOURNAL J. Biol. Chem. 277 (38), 35333-35340 (2002)
 PUBMED [12093792](#)
 REFERENCE 12 (bases 1 to 4484)
 AUTHORS Aganna,E., Martinon,F., Hawkins,P.N., Ross,J.B., Swan,D.C., Booth,D.R., Lachmann,H.J., Bybee,A., Gaudet,R., Woo,P., Feighery,C., Cotter,F.E., Thome,M., Hitman,G.A., Tschopp,J. and McDermott,M.F.
 TITLE Association of mutations in the NALP3/CIAS1/PYPAF1 gene with a broad phenotype including recurrent fever, cold sensitivity, sensorineural deafness, and AA amyloidosis
 JOURNAL Arthritis Rheum. 46 (9), 2445-2452 (2002)
 PUBMED [12355493](#)
 REMARK GeneRIF: Mutations in the NALP3/CIAS1/PYPAF1 gene are associated with familial cold urticaria and Muckle-Wells syndrome.
 REFERENCE 13 (bases 1 to 4484)
 AUTHORS Feldmann,J., Prieur,A.M., Quartier,P., Berquin,P., Certain,S., Cortis,E., Teillac-Hamel,D., Fischer,A. and de Saint Basile,G.
 TITLE Chronic infantile neurological cutaneous and articular syndrome is caused by mutations in CIAS1, a gene highly expressed in polymorphonuclear cells and chondrocytes
 JOURNAL Am. J. Hum. Genet. 71 (1), 198-203 (2002)
 PUBMED [12032915](#)
 REMARK GeneRIF: Chronic infantile neurological cutaneous and articular syndrome is caused by mutations in CIAS1, a gene highly expressed in polymorphonuclear cells and chondrocytes.
 REFERENCE 14 (bases 1 to 4484)
 AUTHORS Srinivasula,S.M., Poyet,J.L., Razmara,M., Datta,P., Zhang,Z. and Alnemri,E.S.
 TITLE The PYRIN-CARD protein ASC is an activating adaptor for caspase-1
 JOURNAL J. Biol. Chem. 277 (24), 21119-21122 (2002)
 PUBMED [11967258](#)
 REFERENCE 15 (bases 1 to 4484)
 AUTHORS Dode,C., Le Du,N., Cuisset,L., Letourneur,F., Berthelot,J.M., Vaudour,G., Meyrier,A., Watts,R.A., Scott,D.G., Nicholls,A., Granel,B., Frances,C., Garcier,F., Edery,P., Boulinguez,S., Domergues,J.P., Delpech,M. and Grateau,G.
 TITLE New mutations of CIAS1 that are responsible for Muckle-Wells syndrome and familial cold urticaria: a novel mutation underlies both syndromes
 JOURNAL Am. J. Hum. Genet. 70 (6), 1498-1506 (2002)
 PUBMED [11992256](#)
 REMARK GeneRIF: New mutations of CIAS1 that are responsible for Muckle-Wells syndrome and familial cold urticaria: a novel mutation underlies both syndromes.
 REFERENCE 16 (bases 1 to 4484)

AUTHORS Manji,G.A., Wang,L., Geddes,B.J., Brown,M., Merriam,S.,
Al-Garawi,A., Mak,S., Lora,J.M., Briskin,M., Jurman,M., Cao,J.,
DiStefano,P.S. and Bertin,J.

TITLE PYPAF1, a PYRIN-containing Apaf1-like protein that assembles with
ASC and regulates activation of NF-kappa B

JOURNAL J. Biol. Chem. 277 (13), 11570-11575 (2002)

PUBMED [11786556](#)

REFERENCE 17 (bases 1 to 4484)

AUTHORS Hoffman,H.M., Mueller,J.L., Broide,D.H., Wanderer,A.A. and
Kolodner,R.D.

TITLE Mutation of a new gene encoding a putative pyrin-like protein
causes familial cold autoinflammatory syndrome and Muckle-Wells
syndrome

JOURNAL Nat. Genet. 29 (3), 301-305 (2001)

PUBMED [11687797](#)

REFERENCE 18 (bases 1 to 4484)

AUTHORS Hoffman,H.M., Wright,F.A., Broide,D.H., Wanderer,A.A. and
Kolodner,R.D.

TITLE Identification of a locus on chromosome 1q44 for familial cold
urticaria

JOURNAL Am. J. Hum. Genet. 66 (5), 1693-1698 (2000)

PUBMED [10741953](#)

COMMENT REVIEWED [REFSEQ](#): This record has been curated by NCBI staff. The
reference sequence was derived from [AF410477.1](#) and [AF054176.1](#).
On Sep 22, 2003 this sequence version replaced [gi:19923283](#).

Summary: This gene encodes a pyrin-like protein which contains a
pyrin domain, a nucleotide-binding site (NBS) domain, and a
leucine-rich repeat (LRR) motif. This protein interacts with
apoptosis-associated speck-like protein containing a CARD. Proteins
which contain the caspase recruitment domain, CARD, have been shown
to be involved in inflammation and immune response. This protein
may function as an activator of NF-kappaB signaling. The encoded
protein may play a role in the regulation of inflammation and
apoptosis. Mutations in this gene have been associated with
familial cold autoinflammatory syndrome (FCAS), Muckle-Wells
syndrome (MWS), chronic infantile neurological cutaneous and
articular (CINCA) syndrome, and neonatal-onset multisystem
inflammatory disease (NOMID). Two transcript variants encoding
distinct isoforms have been identified for this gene.

Transcript Variant: This variant (1) represents the longer
transcript and encodes the longer isoform (a).

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Oct 4 2005 13:52:42



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Display ☒ Show ☒ Send to ☒Range: from to ☐ Reverse complemented strand Features: ☐ SNP ☐ CDD ☒☐ 1: [NM_024618](#). Reports Homo sapiens NOD9...[gi:25777607][Links](#)

LOCUS NM_024618 3761 bp mRNA linear PRI 10-JUN-2005
DEFINITION Homo sapiens NOD9 protein (NOD9), transcript variant 1, mRNA.
ACCESSION NM_024618
VERSION NM_024618.2 GI:25777607
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM [Homo sapiens](#)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 3761)
AUTHORS Inohara,N. and Nunez,G.
TITLE NODs: intracellular proteins involved in inflammation and apoptosis
JOURNAL Nat. Rev. Immunol. 3 (5), 371-382 (2003)
PUBMED [12766759](#)
REMARK Review article
COMMENT REVIEWED REFSEQ: This record has been curated by NCBI staff. The
reference sequence was derived from [BC023974.2](#).
On Nov 27, 2002 this sequence version replaced [gi:13375837](#).

Summary: Alternative splicing has been observed at this gene locus and two transcript variants, encoding distinct isoforms, have been identified. The function of this protein has not been determined.

Transcript Variant: This variant (1) represents the longer transcript and encodes the longer isoform (1).

COMPLETENESS: complete on the 3' end.

FEATURES

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Range: from to ☐ Reverse complemented strand Features: ☐ SNP ☐ CDD ☒

☐ 1: [NM_145827](#). Reports *Mus musculus* cold...[gi:48675839]

Links

LOCUS NM 145827 4022 bp mRNA linear ROD 18-OCT-2005

DEFINITION Mus musculus cold autoinflammatory syndrome 1 homolog (human) (Cias1), mRNA.

ACCESSION NM 145827

VERSION NM 145827.2 GI:48675839

KEYWORDS

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 4022)

AUTHORS Anderson, J.P., Mueller, J.L., Rosengren, S., Boyle, D.L., Schaner, P., Cannon, S.B., Goodyear, C.S. and Hoffman, H.M.

TITLE Structural, expression, and evolutionary analysis of mouse CIAS1

JOURNAL Gene 338 (1), 25-34 (2004)

PUBMED 15302403

REMARK GeneRIF: CIAS1 mRNA expression found primarily in peripheral blood leukocytes consistent with the postulated inflammatory function.

REFERENCE 2 (bases 1 to 4022)

AUTHORS Kikuchi-Yanoshita, R., Taketomi, Y., Koga, K., Sugiki, T., Atsumi, Y., Saito, T., Ishii, S., Hisada, M., Suzuki-Nishimura, T., Uchida, M.K., Moon, T.C., Chang, H.W., Sawada, M., Inagaki, N., Nagai, H., Murakami, M. and Kudo, I.

TITLE Induction of PYPAF1 during in vitro maturation of mouse mast cells

JOURNAL J. Biochem. 134 (5), 699-709 (2003)

PUBMED 14688236

REMARK GeneRIF: MMIG-1, a likely mouse PYPAF1 ortholog, may play a role in mast cell-directed inflammatory diseases

REFERENCE 3 (bases 1 to 4022)

AUTHORS Albrecht, M., Domingues, F.S., Schreiber, S. and Lengauer, T.

TITLE Identification of mammalian orthologs associates PYPAF5 with distinct functional roles

JOURNAL FEBS Lett. 538 (1-3), 173-177 (2003)

PUBMED 12633874

COMMENT PROVISIONAL REFSEQ: This record has not yet been subject to final
NCBI review. The reference sequence was derived from AY495376.1.
On Jun 13, 2004 this sequence version replaced gi:22003869.

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Range: from to ☐ Reverse complemented strand Features: ☐ SNP ☐ CDD ☒

□ 1: [NM_170722](#). Reports *Homo sapiens* NOD9...[gi:25777609]

Links

LOCUS NM 170722 3055 bp mRNA linear PRI 10-JUN-2005

DEFINITION Homo sapiens NOD9 protein (NOD9), transcript variant 2, mRNA.

ACCESSION NM 170722

VERSION NM 170722.1 GI:25777609

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1 (bases 1 to 3055)

AUTHORS Inohara, N. and Nunez, G.

TITLE NODs: intracellular proteins involved in inflammation and apoptosis

JOURNAL Nat. Rev. Immunol. 3 (5), 371-382 (2003)

PUBMED 12766759

REMARK Review article

COMMENT REVIEWED REFSEQ: This record has been curated by NCBI staff. The reference sequence was derived from BC013199.1 and BC023974.2.

Summary: Alternative splicing has been observed at this gene locus and two transcript variants, encoding distinct isoforms, have been identified. The function of this protein has not been determined.

Transcript Variant: This variant (2) uses an alternate splice site for the 3' terminal exon, resulting in a missing internal segment compared to variant 1. The encoded isoform (2) has a shorter and distinct C-terminus compared to isoform 1.

COMPLETENESS: complete on the 3' end.

FEATURES

source

Location/Qualifiers

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☐ 1: NT_009325[gi:29746596] This record was removed as a result of standard genome annotation processing. See the genome build documentation at <http://www.ncbi.nlm.nih.gov/genome/guide/build.html> for further information, or contact info@ncbi.nlm.nih.gov.

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 ACCESSION NT_009325
 VERSION NT_009325.14 GI:29746596
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 2818927)
 AUTHORS International Human Genome Sequencing Consortium.
 TITLE The DNA sequence of Homo sapiens
 JOURNAL Unpublished (2003)
 COMMENT GENOME ANNOTATION REFSEQ: NCBI contigs are derived from assembled
 genomic sequence data.
 Also see:
[Documentation of NCBI's Annotation Process](#)

On Apr 10, 2003 this sequence version replaced gi:27499439.
 This contig has been assembled by NCBI staff from individual clone
 sequences making use of a tiling path supplied by the sequencing
 centers.

COMPLETENESS: not full length.

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STS 81037..81232
      /standard_name="D11S2349"
      /note="WARNING: map location ambiguous"
      /db_xref="UniSTS:151812"
gene 85543..100398
      /gene="LOC120800"
      /db_xref="InterimID:120800"
mRNA join(85543..86484,100285..100398)
      /gene="LOC120800"
      /product="similar to seven transmembrane helix receptor
[Homo sapiens]"
      /note="Derived by automated computational analysis using
gene prediction method: GenomeScan."
      /transcript_id="XM_062276.3"
      /db_xref="GI:27499404"
      /db_xref="InterimID:120800"
CDS join(85543..86484,100285..100398)
      /gene="LOC120800"
      /codon_start=1
      /protein_id="XP_062276.3"
      /db_xref="GI:27499405"
      /db_xref="InterimID:120800"
STS 102817..103168
      /standard_name="G54605"
      /note="WARNING: map location ambiguous"
      /db_xref="UniSTS:117740"
STS 102818..103092
      /standard_name="G60067"
      /note="WARNING: map location ambiguous"
      /db_xref="UniSTS:137328"
gene complement(106163..107104)
      /gene="LOC120799"
      /db_xref="InterimID:120799"
mRNA complement(106163..107104)
      /gene="LOC120799"
      /product="similar to Olfactory receptor 52E6"
      /note="Derived by automated computational analysis using
gene prediction method: GenomeScan."

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/ transcript_id="XM_062275.3"
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/ db_xref="InterimID:120799"
CDS complement(106163..107104)
/ gene="LOC120799"
/ codon_start=1
/ protein_id="XP_062275.3"
/ db_xref="GI:27499407"
/ db_xref="InterimID:120799"
gene complement(121956..122699)
/ gene="LOC203960"
/ db_xref="InterimID:203960"
mRNA complement(121956..122699)
/ gene="LOC203960"
/ product="similar to Olfactory receptor 52E6"
/ note="Derived by automated computational analysis using
gene prediction method: GenomeScan."
/ transcript_id="XM_115089.1"
/ db_xref="GI:20486166"
/ db_xref="InterimID:203960"
CDS complement(121956..122699)
/ gene="LOC203960"
/ codon_start=1
/ protein_id="XP_115089.1"
/ db_xref="GI:20486167"
/ db_xref="InterimID:203960"
gene 139501..140016
/ gene="LOC283290"
/ db_xref="InterimID:283290"
mRNA join(139501..139565,139590..140016)
/ gene="LOC283290"
/ product="similar to olfactory receptor MOR32-1 [Mus
musculus]"
/ note="Derived by automated computational analysis using
gene prediction method: GenomeScan."
/ transcript_id="XM_210222.1"
/ db_xref="GI:27499408"
/ db_xref="InterimID:283290"
CDS join(139501..139565,139590..140016)
/ gene="LOC283290"
/ codon_start=1
/ protein_id="XP_210222.1"
/ db_xref="GI:27499409"
/ db_xref="InterimID:283290"
gene 149500..150438
/ gene="LOC283291"
/ db_xref="InterimID:283291"
mRNA 149500..150438
/ gene="LOC283291"
/ product="similar to olfactory receptor MOR32-11 [Mus
musculus]"
/ note="Derived by automated computational analysis using
gene prediction method: GenomeScan."
/ transcript_id="XM_210223.1"
/ db_xref="GI:27499410"
/ db_xref="InterimID:283291"
CDS 149500..150438
/ gene="LOC283291"
/ codon_start=1
/ protein_id="XP_210223.1"

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gene 155415..213498
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     /db_xref="InterimID:341274"
mRNA join(155415..155556,166087..166883,169072..169191,
     193877..194148,209483..209664,212681..213498)
     /gene="LOC341274"
     /product="similar to seven transmembrane helix receptor
[Homo sapiens]"
     /note="Derived by automated computational analysis using
gene prediction method: GenomeScan."
     /transcript_id="XM_291976.1"
     /db_xref="GI:29746582"
     /db_xref="InterimID:341274"
CDS join(155415..155556,166087..166883,169072..169191,
     193877..194148,209483..209664,212681..213498)
     /gene="LOC341274"
     /codon_start=1
     /protein_id="XP_291976.1"
     /db_xref="GI:29746583"
     /db_xref="InterimID:341274"
STS 231950..232206
     /standard_name="D11S1338"
     /db_xref="UniSTS:43509"
STS 232004..232203
     /standard_name="D11S1338"
     /db_xref="UniSTS:64797"
gene complement(232757..233575)
     /gene="LOC255723"
     /db_xref="InterimID:255723"
mRNA complement(232757..233575)
     /gene="LOC255723"
     /product="similar to seven transmembrane helix receptor
[Homo sapiens]"
     /note="Derived by automated computational analysis using
gene prediction method: GenomeScan."
     /transcript_id="XM_171526.1"
     /db_xref="GI:22066607"
     /db_xref="InterimID:255723"
CDS complement(232757..233575)
     /gene="LOC255723"
     /codon_start=1
     /protein_id="XP_171526.1"
     /db_xref="GI:22066608"
     /db_xref="InterimID:255723"
gene complement(251145..253923)
     /gene="LOC338751"
     /db_xref="InterimID:338751"
mRNA complement(join(251145..252034,253917..253923))
     /gene="LOC338751"
     /product="similar to seven transmembrane helix receptor
[Homo sapiens]"
     /note="Derived by automated computational analysis using
gene prediction method: GenomeScan."
     /transcript_id="XM_291977.1"
     /db_xref="GI:29746567"
     /db_xref="InterimID:338751"
CDS complement(join(251145..252034,253917..253923))
     /gene="LOC338751"

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/codon_start=1
/protein_id="XP_291977.1"
/db_xref="GI:29746568"
/db_xref="InterimID:338751"
gene complement(259078..268196)
/gene="LOC120793"
/db_xref="InterimID:120793"
mRNA complement(join(259078..259178,259263..259370,
259509..259974,260199..260364,267259..268196))
/gene="LOC120793"
/product="similar to seven transmembrane helix receptor
[Homo sapiens]"
/note="Derived by automated computational analysis using
gene prediction method: GenomeScan."
/transcript_id="XM_062269.6"
/db_xref="GI:29746569"
/db_xref="InterimID:120793"
CDS complement(join(259078..259178,259263..259370,
259509..259974,260199..260364,267259..268196))
/gene="LOC120793"
/codon_start=1
/protein_id="XP_062269.6"
/db_xref="GI:29746570"
/db_xref="InterimID:120793"
STS 264685..265010
/standard_name="G63178"
/db_xref="UniSTS:140295"
STS 268806..269035
/standard_name="D11S2415"
/db_xref="UniSTS:71983"
STS 269961..270275
/standard_name="RH123738"
/db_xref="UniSTS:137759"
STS 269961..270273
/standard_name="SHGC-68742"
/db_xref="UniSTS:95528"
gene complement(291952..292896)
/gene="LOC120796"
/db_xref="InterimID:120796"
mRNA complement(291952..292896)
/gene="LOC120796"
/product="similar to seven transmembrane helix receptor
[Homo sapiens]"
/note="Derived by automated computational analysis using
gene prediction method: GenomeScan."
/transcript_id="XM_062272.7"
/db_xref="GI:29746571"
/db_xref="InterimID:120796"
CDS complement(291952..292896)
/gene="LOC120796"
/codon_start=1
/protein_id="XP_062272.7"
/db_xref="GI:29746572"
/db_xref="InterimID:120796"
gene complement(311166..325389)
/gene="LOC196338"
/db_xref="InterimID:196338"
mRNA complement(join(311166..311751,322524..323379,
325380..325389))
/gene="LOC196338"

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/product="similar to seven transmembrane helix receptor
[Homo sapiens]"
/note="Derived by automated computational analysis using
gene prediction method: GenomeScan."
/transcript_id="XM_115093.3"
/db_xref="GI:27499418"
/db_xref="InterimID:196338"
CDS      complement(join(311166..311751,322524..323379,
325380..325389))
/gene="LOC196338"
/codon_start=1
/protein_id="XP_115093.3"
/db_xref="GI:27499419"
/db_xref="InterimID:196338"
gene      complement(332017..332996)
/gene="OR52X1P"
/pseudo
/db_xref="LocusID:79272"
misc_feature 348970..535573
/standard_name="RP11-290F24"
/note="FISH-mapped clone"
STS      364652..364866
/standard_name="D11S1241"
/db_xref="UniSTS:148332"
gene      372983..373942
/gene="LOC196335"
/db_xref="InterimID:196335"
mRNA      372983..373942
/gene="LOC196335"
/product="similar to olfactory receptor MOR40-3 [Mus
musculus]"
/note="Derived by automated computational analysis using
gene prediction method: GenomeScan."
/transcript_id="XM_115092.2"
/db_xref="GI:29746573"
/db_xref="InterimID:196335"
CDS      372983..373942
/gene="LOC196335"
/codon_start=1
/protein_id="XP_115092.1"
/db_xref="GI:20486038"
/db_xref="InterimID:196335"
STS      390560..390830
/standard_name="SHGC-106674"
/db_xref="UniSTS:169983"
misc_feature 392790..520892
/standard_name="RP11-98L18"
/note="FISH-mapped clone"
gene      394045..394700
/gene="LOC120790"
/db_xref="InterimID:120790"
mRNA      join(394045..394447,394666..394700)
/gene="LOC120790"
/product="similar to seven transmembrane helix receptor
[Homo sapiens]"
/note="Derived by automated computational analysis using
gene prediction method: GenomeScan."
/transcript_id="XM_062266.2"
/db_xref="GI:29746574"
/db_xref="InterimID:120790"

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CDS join(394045..394447,394666..394700)
/gene="LOC120790"
/codon_start=1
/protein_id="XP_062266.2"
/db_xref="GI:29746575"
/db_xref="InterimID:120790"

STS 396334..396444
/standard_name="D11S3090"
/db_xref="UniSTS:152185"

gene complement(416887..417395)
/gene="LOC144133"
/db_xref="InterimID:144133"

mRNA complement(416887..417395)
/gene="LOC144133"
/product="similar to seven transmembrane helix receptor [Homo sapiens]"
/note="Derived by automated computational analysis using gene prediction method: BLAST. Supporting evidence includes similarity to: 1 mRNA"
/transcript_id="XM_084743.1"
/db_xref="GI:18605356"
/db_xref="InterimID:144133"

CDS complement(416980..417345)
/gene="LOC144133"
/codon_start=1
/protein_id="XP_084743.1"
/db_xref="GI:18605357"
/db_xref="InterimID:144133"

gene complement(434559..435530)
/gene="LOC255725"
/db_xref="InterimID:255725"

mRNA complement(434559..435530)
/gene="LOC255725"
/product="similar to Olfactory receptor 52B2"
/note="Derived by automated computational analysis using gene prediction method: GenomeScan."
/transcript_id="XM_171528.1"
/db_xref="GI:22066626"
/db_xref="InterimID:255725"

CDS complement(434559..435530)
/gene="LOC255725"
/codon_start=1
/protein_id="XP_171528.1"
/db_xref="GI:22066627"
/db_xref="InterimID:255725"

gene 464428..465390
/gene="LOC120787"
/db_xref="InterimID:120787"

mRNA 464428..465390
/gene="LOC120787"
/product="similar to olfactory receptor MOR36-1 [Mus musculus]"
/note="Derived by automated computational analysis using gene prediction method: GenomeScan."
/transcript_id="XM_062263.1"
/db_xref="GI:17461543"
/db_xref="InterimID:120787"

CDS 464428..465390
/gene="LOC120787"
/codon_start=1

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/protein_id="XP_062263.1"
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/db_xref="InterimID:120787"
STS 467206..467343
/standard_name="G31000"
/db_xref="UniSTS:28049"
gene 470772..476333
/gene="MGC34805"
/db_xref="LocusID:160298"
mRNA join(470772..470891,475054..475852,476116..476333)
/gene="MGC34805"
/product="hypothetical protein MGC34805"
/note="unclassified transcription discrepancy; Derived by
automated computational analysis using gene prediction
method: BestRefseq,BLAST. Supporting evidence includes
similarity to: 2 mRNAs"
/transcript_id="NM_173525.1"
/db_xref="GI:27734960"
/db_xref="LocusID:160298"
CDS join(470820..470891,475054..475852,476116..476246)
/gene="MGC34805"
/note="unclassified translation discrepancy"
/codon_start=1
/evidence=not_experimental
/product="hypothetical protein MGC34805"
/protein_id="NP_775796.1"
/db_xref="GI:27734961"
/db_xref="LocusID:160298"
gene complement(476541..499867)
/gene="DKFZP566M1046"
/db_xref="LocusID:84067"
mRNA complement(join(476551..477071,479615..479777,
479937..480115,482575..483354,483762..483967,
484175..484254,487646..487813,488015..488101,
488284..488442,488814..489452,489583..489911,
499748..499849))
/gene="DKFZP566M1046"
/product="hypothetical protein DKFZp566M1046"
/note="unclassified transcription discrepancy; Derived by
automated computational analysis using gene prediction
method: BestRefseq,BLAST. Supporting evidence includes
similarity to: 1 mRNA"
/transcript_id="NM_032127.1"
/db_xref="GI:14149782"
/db_xref="LocusID:84067"
CDS complement(join(476710..477071,479615..479777,
479937..480115,482575..483354,483762..483967,
484175..484254,487646..487813,488015..488101,
488284..488442,488814..489452,489583..489720))
/gene="DKFZP566M1046"
/note="similarity to C.elegans C05D11.8; unclassified
translation discrepancy"
/codon_start=1
/product="hypothetical protein DKFZp566M1046"
/protein_id="NP_115503.1"
/db_xref="GI:14149783"
/db_xref="LocusID:84067"
STS 480870..481044
/standard_name="G20710;A006C42"
/db_xref="UniSTS:68786"

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STS      /db_xref="UniSTS:68787"
         491270..491403
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         /db_xref="UniSTS:54740"
gene     500098..509681
         /gene="LOC338753"
         /db_xref="InterimID:338753"
mRNA     join(500098..500213,504588..504689,504888..504994,
         505270..505915,506635..509681)
         /gene="LOC338753"
         /product="similar to Cyclic nucleotide gated cation
channel; olfactory cyclic nucleotide-gated channel [Rattus
norvegicus]"
         /note="Derived by automated computational analysis using
gene prediction method: BLAST. Supporting evidence
includes similarity to: 1 mRNA"
         /transcript_id="XM_290552.1"
         /db_xref="GI:29746576"
         /db_xref="InterimID:338753"
CDS      join(504646..504689,504888..504994,505270..505915,
         506635..507088)
         /gene="LOC338753"
         /codon_start=1
         /protein_id="XP_290552.1"
         /db_xref="GI:29746577"
         /db_xref="InterimID:338753"
misc_feature 520658..520892
         /standard_name="RP11-645I8"
         /note="FISH-mapped clone"
misc_feature 520658..520791
         /standard_name="RP11-149K16"
         /note="FISH-mapped clone"
STS      520658..520791
         /standard_name="D11S1323"
         /db_xref="UniSTS:67612"
STS      520688..520892
         /standard_name="D11S1323"
         /db_xref="UniSTS:72457"
STS      522183..522469
         /standard_name="SHGC-111644"
         /db_xref="UniSTS:168453"
gene     524947..537329
         /gene="CCKBR"
         /db_xref="LocusID:887"
         /db_xref="MIM:118445"
mRNA     join(525130..525283,534873..535124,535292..535541,
         535850..537329)
         /gene="CCKBR"
         /product="cholecystokinin B receptor"
         /note="unclassified transcription discrepancy; Derived by
automated computational analysis using gene prediction
method: BestRefseq,BLAST. Supporting evidence includes
similarity to: 1 mRNA"
         /transcript_id="NM_000731.2"
         /db_xref="GI:21361152"
         /db_xref="LocusID:887"
         /db_xref="MIM:118445"
CDS      join(525133..525283,534873..535124,535292..535541,
         535850..536747)
         /gene="CCKBR"

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  /protein_id="NP_000722.2"
  /db_xref="GI:21361153"
  /db_xref="LocusID:887"
  /db_xref="MIM:118445"
  STS 537249..537459
    /standard_name="RH69002"
    /db_xref="UniSTS:66177"
  misc_feature 557896..718429
    /standard_name="RP11-30I3"
    /note="FISH-mapped clone"
  gene complement(584152..585851)
    /gene="PRKCDBP"
    /db_xref="LocusID:112464"
  mRNA complement(join(584152..584768,585297..585714))
    /gene="PRKCDBP"
    /product="protein kinase C, delta binding protein"
    /note="unclassified transcription discrepancy; Derived by
    automated computational analysis using gene prediction
    method: BestRefseq,BLAST. Supporting evidence includes
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    /db_xref="GI:21450786"
    /db_xref="LocusID:112464"
  STS 584152..584391
    /standard_name="RH80357"
    /db_xref="UniSTS:87546"
  STS 584165..584299
    /standard_name="RH103676"
    /db_xref="UniSTS:98001"
  STS 584264..584407
    /standard_name="STS-AA030008"
    /db_xref="UniSTS:58285"
  CDS complement(join(584367..584768,585297..585680))
    /gene="PRKCDBP"
    /note="unclassified translation discrepancy"
    /codon_start=1
    /product="protein kinase C, delta binding protein"
    /protein_id="NP_659477.1"
    /db_xref="GI:21450787"
    /db_xref="LocusID:112464"
  gene 589235..645662
    /gene="LOC341275"
    /db_xref="InterimID:341275"
  mRNA join(589235..589239,594769..594837,598041..598102,
  628274..628491,645432..645662)
    /gene="LOC341275"
    /product="LOC341275"
    /note="Derived by automated computational analysis using
    gene prediction method: GenomeScan."
    /transcript_id="XM_296082.1"
    /db_xref="GI:29746584"
    /db_xref="InterimID:341275"
  CDS join(589235..589239,594769..594837,598041..598102,
  628274..628491,645432..645662)
    /gene="LOC341275"
    /codon_start=1
    /protein_id="XP_296082.1"

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/db_xref="GI:29746585"
/db_xref="InterimID:341275"
STS 600036..600175
     /gene="LOC341275"
     /standard_name="RH92838"
     /db_xref="UniSTS:85687"
STS 602093..602296
     /gene="LOC341275"
     /standard_name="D11S1997"
     /db_xref="UniSTS:82667"
STS 609826..609949
     /gene="LOC341275"
     /standard_name="RH92043"
     /db_xref="UniSTS:85957"
STS 610489..610663
     /gene="LOC341275"
     /standard_name="D11S4034"
     /db_xref="UniSTS:21496"
misc_feature 654687..655117
             /standard_name="RP11-93A12"
             /note="FISH-mapped clone"
gene 655536..660199
     /gene="SMPD1"
     /db_xref="LocusID:6609"
     /db_xref="MIM:257200"
STS 655762..655958
     /gene="SMPD1"
     /standard_name="STS-M81780"
     /db_xref="UniSTS:12276"
mRNA join(655803..656120,656588..657360,658420..658591,
        658821..658897,659100..659245,659402..659811)
     /gene="SMPD1"
     /product="sphingomyelin phosphodiesterase 1, acid
lysosomal (acid sphingomyelinase)"
     /note="unclassified transcription discrepancy; Derived by
automated computational analysis using gene prediction
method: BestRefseq,BLAST. Supporting evidence includes
similarity to: 1 mRNA"
     /transcript_id="NM_000543.1"
     /db_xref="GI:4507092"
     /db_xref="LocusID:6609"
     /db_xref="MIM:257200"
CDS join(655803..656120,656588..657360,658420..658591,
        658821..658897,659100..659245,659402..659805)
     /gene="SMPD1"
     /EC_number="3.1.4.12"
     /note="unclassified translation discrepancy; sphingomyelin
phosphodiesterase-1, acid lysosomal"
     /codon_start=1
     /product="sphingomyelin phosphodiesterase 1, acid
lysosomal (acid sphingom"
     /protein_id="NP_000534.1"
     /db_xref="GI:4507093"
     /db_xref="LocusID:6609"
     /db_xref="MIM:257200"
STS 656338..656505
     /gene="SMPD1"
     /standard_name="RH69187"
     /db_xref="UniSTS:66320"
STS 659827..660152

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/ gene="SMPD1"
/ standard_name="D11S4426"
/ db_xref="UniSTS:21687"
STS      659864..660075
/ gene="SMPD1"
/ standard_name="SMPD1"
/ db_xref="UniSTS:48627"
gene      complement(660329..684618)
/ gene="APBB1"
/ db_xref="LocusID:322"
/ db_xref="MIM:602709"
mRNA      complement(join(660329..660905,660990..661166,
661304..661419,666193..666276,666549..666633,
666778..666892,667286..667413,667780..667929,
668349..668412,668523..668608,668692..668748,
668851..669026,675831..676565,684550..684618))
/ gene="APBB1"
/ product="amyloid beta (A4) precursor protein-binding,
family B, member 1 (Fe65)"
/ note="unclassified transcription discrepancy; Derived by
automated computational analysis using gene prediction
method: BestRefseq,BLAST. Supporting evidence includes
similarity to: 4 mRNAs"
/ transcript_id="NM_145689.1"
/ db_xref="GI:22035553"
/ db_xref="LocusID:322"
/ db_xref="MIM:602709"
mRNA      complement(join(660329..660905,660990..661166,
661304..661419,666193..666276,666549..666633,
666778..666892,667283..667413,667780..667929,
668349..668412,668523..668608,668692..668748,
668851..669026,675831..676565,684189..684274))
/ gene="APBB1"
/ product="amyloid beta (A4) precursor protein-binding,
family B, member 1 (Fe65)"
/ note="unclassified transcription discrepancy; Derived by
automated computational analysis using gene prediction
method: BestRefseq,BLAST. Supporting evidence includes
similarity to: 1 mRNA"
/ transcript_id="NM_001164.2"
/ db_xref="GI:22035552"
/ db_xref="LocusID:322"
/ db_xref="MIM:602709"
STS      660354..660566
/ standard_name="A002D29"
/ db_xref="UniSTS:17869"
CDS      complement(join(660738..660905,660990..661166,
661304..661419,666193..666276,666549..666633,
666778..666892,667286..667413,667780..667929,
668349..668412,668523..668608,668692..668748,
668851..669026,675831..676551))
/ gene="APBB1"
/ note="amyloid beta A4 precursor protein-binding, family
B, member 1; stat-like protein; adaptor protein FE65a2"
/ codon_start=1
/ product="amyloid beta A4 precursor protein-binding,
family B, member 1 isoform delta E9"
/ protein_id="NP_663722.1"
/ db_xref="GI:22035554"
/ db_xref="LocusID:322"

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CDS /db_xref="MIM:602709"
 complement(join(660738..660905;660990..661166,
 661304..661419,666193..666276,666549..666633,
 666778..666892,667283..667413,667780..667929,
 668349..668412,668523..668608,668692..668748,
 668851..669026,675831..676551))
 /gene="APBB1"
 /note="unclassified translation discrepancy; amyloid beta
 A4 precursor protein-binding, family B, member 1;
 stat-like protein; adaptor protein FE65a2"
 /codon_start=1
 /product="amyloid beta A4 precursor protein-binding,
 family B, member 1 isoform E9"
 /protein_id="NP_001155.1"
 /db_xref="GI:4502131"
 /db_xref="LocusID:322"
 /db_xref="MIM:602709"
 STS 665795..665910
 /standard_name="G63687"
 /db_xref="UniSTS:140649"
 gene complement(696255..707790)
 /gene="HPX"
 /db_xref="LocusID:3263"
 /db_xref="MIM:142290"
 STS 696285..696407
 /standard_name="D11S4588"
 /db_xref="UniSTS:68264"
 mRNA complement(join(696415..696674,696845..697007,
 697091..697221,702249..702380,702643..702855,
 703559..703712,705368..705489,705670..705741,
 705863..705921,706072..706154))
 /gene="HPX"
 /product="hemopexin"
 /note="Derived by automated computational analysis using
 gene prediction method: BestRefseq,BLAST. Supporting
 evidence includes similarity to: 1 mRNA"
 /transcript_id="NM_000613.1"
 /db_xref="GI:11321560"
 /db_xref="LocusID:3263"
 /db_xref="MIM:142290"
 CDS complement(join(696415..696674,696845..697007,
 697091..697221,702249..702380,702643..702855,
 703559..703712,705368..705489,705670..705741,
 705863..705921,706072..706154))
 /gene="HPX"
 /note="precursor"
 /codon_start=1
 /product="hemopexin"
 /protein_id="NP_000604.1"
 /db_xref="GI:11321561"
 /db_xref="LocusID:3263"
 /db_xref="MIM:142290"
 STS 705708..706162
 /standard_name="GDB:197845"
 /db_xref="UniSTS:155963"
 gene complement(713807..739180)
 /gene="TRIM3"
 /db_xref="LocusID:10612"
 /db_xref="MIM:605493"
 STS 713826..714010

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/standard_name="RH71141"
/db_xref="UniSTS:60910"
STS 713826..713961
/standard_name="RH47384"
/db_xref="UniSTS:60909"
STS 713826..713953
/standard_name="SGC34546"
/db_xref="UniSTS:60911"
mRNA complement(join(714196..714373,714499..714639,
715744..715814,716085..716253,716464..716631,
721265..721368,721490..722014,722518..722669,
722889..723040,723258..723489,730758..730888))
/gene="TRIM3"
/product="tripartite motif-containing 3"
/note="unclassified transcription discrepancy; Derived by
automated computational analysis using gene prediction
method: BestRefseq,BLAST. Supporting evidence includes
similarity to: 1 mRNA"
/transcript_id="NM_033279.1"
/db_xref="GI:15451754"
/db_xref="LocusID:10612"
/db_xref="MIM:605493"
mRNA complement(join(714196..714373,714499..714639,
715744..715814,716085..716253,716464..716631,
721265..721368,721490..722222,722489..722669,
722889..723040,723258..723489,730758..730888))
/gene="TRIM3"
/product="tripartite motif-containing 3"
/note="unclassified transcription discrepancy; Derived by
automated computational analysis using gene prediction
method: BestRefseq,BLAST. Supporting evidence includes
similarity to: 2 mRNAs"
/transcript_id="NM_006458.1"
/db_xref="GI:5453568"
/db_xref="LocusID:10612"
/db_xref="MIM:605493"
CDS complement(join(714221..714373,714499..714639,
715744..715814,716085..716253,716464..716631,
721265..721368,721490..722014,722518..722669,
722889..723040,723258..723489,730758..730888))
/gene="TRIM3"
/note="unclassified translation discrepancy; brain
expressed ring finger; tripartite motif protein TRIM3;
ring finger protein 22"
/codon_start=1
/product="tripartite motif-containing 3 isoform gamma"
/protein_id="NP_150595.1"
/db_xref="GI:15451755"
/db_xref="LocusID:10612"
/db_xref="MIM:605493"
CDS complement(join(714221..714373,714499..714639,
715744..715814,716085..716253,716464..716631,
721265..721368,721490..722222,722489..722669,
722889..723040,723258..723489,730758..730888))
/gene="TRIM3"
/note="unclassified translation discrepancy; brain
expressed ring finger; tripartite motif protein TRIM3"
/codon_start=1
/product="ring finger protein 22, isoform alpha"
/protein_id="NP_006449.1"

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/db_xref="GI:5453569"
/db_xref="LocusID:10612"
/db_xref="MIM:605493"
STS 721548..721721
     /standard_name="RH12618"
     /db_xref="UniSTS:89873"
STS 733994..734146
     /standard_name="D11S4905"
     /db_xref="UniSTS:76599"
STS 735340..735489
     /standard_name="D11S2391"
     /db_xref="UniSTS:50314"
STS 735357..735483
     /standard_name="RH91168"
     /db_xref="UniSTS:85551"
STS 735367..735479
     /standard_name="D11S2266E"
     /db_xref="UniSTS:46848"
STS 735378..735501
     /standard_name="SHGC-30684"
     /db_xref="UniSTS:6728"
STS 739925..740175
     /standard_name="WI-22461"
     /db_xref="UniSTS:48639"
STS 739926..739997
     /standard_name="STS-Z40796"
     /db_xref="UniSTS:31171"
STS 741731..741920
     /standard_name="IB2126"
     /db_xref="UniSTS:78484"
gene complement(741745..746532)
     /gene="POR1"
     /db_xref="LocusID:23647"
     /db_xref="MIM:601638"
mRNA complement(join(741745..742461,742911..743085,
743234..743391,743931..744152,744333..744451,
745165..745261,745516..745616,746424..746488))
     /gene="POR1"
     /product="partner of RAC1 (arfaptin 2)"
     /note="unclassified transcription discrepancy; Derived by
automated computational analysis using gene prediction
method: BestRefseq,BLAST. Supporting evidence includes
similarity to: 1 mRNA"
     /transcript_id="NM_012402.1"
     /db_xref="GI:6912601"
     /db_xref="LocusID:23647"
     /db_xref="MIM:601638"
STS 741770..741897
     /standard_name="RH11646"
     /db_xref="UniSTS:23650"
CDS complement(join(742306..742461,742911..743085,
743234..743391,743931..744152,744333..744451,
745165..745261,745516..745614))
     /gene="POR1"
     /codon_start=1
     /product="partner of RAC1 (arfaptin 2)"
     /protein_id="NP_036534.1"
     /db_xref="GI:6912602"
     /db_xref="LocusID:23647"
     /db_xref="MIM:601638"

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gene      746656..749873
          /gene="FXC1"
          /db_xref="LocusID:26515"
          /db_xref="MIM:607388"
mRNA      join(746656..746748,746950..747045,747238..748514)
          /gene="FXC1"
          /product="fracture callus 1 homolog (rat)"
          /note="unclassified transcription discrepancy; Derived by
          automated computational analysis using gene prediction
          method: BestRefseq, BLAST. Supporting evidence includes
          similarity to: 6 mRNAs"
          /transcript_id="NM_012192.1"
          /db_xref="GI:6912381"
          /db_xref="LocusID:26515"
          /db_xref="MIM:607388"
CDS       join(746711..746748,746950..747045,747238..747414)
          /gene="FXC1"
          /note="putatively involved in mitochondrial carrier import
          into the inner membrane; similar to yeast Tim9; similar to
          the Tim10/Tim12/DDP protein family; unclassified
          translation discrepancy; fracture callus 1 (rat) homolog"
          /codon_start=1
          /product="fracture callus 1 homolog"
          /protein_id="NP_036324.1"
          /db_xref="GI:6912382"
          /db_xref="LocusID:26515"
          /db_xref="MIM:607388"
STS       748047..748189
          /gene="FXC1"
          /standard_name="RH103170"
          /db_xref="UniSTS:97503"
STS       756313..756411
          /standard_name="SHGC-57652"
          /db_xref="UniSTS:53802"
misc_feature 760537..929997
          /standard_name="RP11-8906"
          /note="FISH-mapped clone"
gene      762453..769393
          /gene="LOC283293"
          /db_xref="InterimID:283293"
mRNA      join(762453..762524,762778..762860,763916..764154,
          767946..769393)
          /gene="LOC283293"
          /product="LOC283293"
          /note="Derived by automated computational analysis using
          gene prediction method: BLAST. Supporting evidence
          includes similarity to: 1 mRNA"
          /transcript_id="XM_210962.1"
          /db_xref="GI:27499422"
          /db_xref="InterimID:283293"
CDS       768095..768391
          /gene="LOC283293"
          /codon_start=1
          /protein_id="XP_210962.1"
          /db_xref="GI:27499423"
          /db_xref="InterimID:283293"
gene      773406..786051
          /gene="FLJ35709"
          /db_xref="LocusID:283294"
mRNA      join(773406..774276,774355..774465,776466..776622,

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784793..785047,785158..786051)
/gene="FLJ35709"
/product="hypothetical protein FLJ35709"
/note="unclassified transcription discrepancy; Derived by
automated computational analysis using gene prediction
method: BestRefseq,BLAST. Supporting evidence includes
similarity to: 2 mRNAs"
/transcript_id="NM_173589.1"
/db_xref="GI:27734792"
/db_xref="LocusID:283294"
CDS
join(774086..774276,774355..774465,776466..776622,
784793..785047,785158..785304)
/gene="FLJ35709"
/codon_start=1
/evidence=not_experimental
/product="hypothetical protein FLJ35709"
/protein_id="NP_775860.1"
/db_xref="GI:27734793"
/db_xref="LocusID:283294"
STS
791393..791637
/standard_name="D11S4585"
/db_xref="UniSTS:34466"
gene
799117..814228
/gene="LOC196337"
/db_xref="InterimID:196337"
mRNA
join(799117..799422,803576..803703,803805..804003,
804412..804506,805069..805276,809314..809439,
809767..809864,810070..812859,813056..813595,
813838..814228)
/gene="LOC196337"
/product="similar to FLJ00251 protein [Homo sapiens]"
/note="Derived by automated computational analysis using
gene prediction method: BLAST. Supporting evidence
includes similarity to: 2 mRNAs"
/transcript_id="XM_113696.1"
/db_xref="GI:20486053"
/db_xref="InterimID:196337"
CDS
join(810159..812859,813056..813273)
/gene="LOC196337"
/codon_start=1
/protein_id="XP_113696.1"
/db_xref="GI:20486054"
/db_xref="InterimID:196337"
STS
814086..814210
/gene="LOC196337"
/standard_name="WI-11771"
/db_xref="UniSTS:79547"
STS
814885..815009
/standard_name="WI-14280"
/db_xref="UniSTS:63605"
gene
829630..837212
/gene="FLJ32752"
/db_xref="LocusID:144132"
mRNA
join(831298..831586,831780..831958,832088..833053,
833249..833435,833647..833769,833858..834059,
835202..835293,835440..835589,835811..836616,
836829..837212)
/gene="FLJ32752"
/product="hypothetical protein FLJ32752"
/note="unclassified transcription discrepancy; Derived by

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automated computational analysis using gene prediction
 method: BestRefseq,BLAST. Supporting evidence includes
 similarity to: 1 mRNA
 /transcript_id="NM_144666.1"
 /db_xref="GI:21389554"
 /db_xref="LocusID:144132"
 CDS join(831577..831586,831780..831958,832088..833053,
 833249..833435,833647..833769,833858..834059,
 835202..835293,835440..835589,835811..836616,
 836829..837179)
 /gene="FLJ32752"
 /codon_start=1
 /evidence=not_experimental
 /product="hypothetical protein FLJ32752"
 /protein_id="NP_653267.1"
 /db_xref="GI:21389555"
 /db_xref="LocusID:144132"
 STS 836965..837149
 /gene="FLJ32752"
 /standard_name="RH99124"
 /db_xref="UniSTS:87363"
 STS 853653..853781
 /standard_name="WI-17590"
 /db_xref="UniSTS:36616"
 gene complement(857572..860245)
 /gene="LOC283295"
 /db_xref="InterimID:283295"
 mRNA complement(857572..860245)
 /gene="LOC283295"
 /product="LOC283295"
 /note="Derived by automated computational analysis using
 gene prediction method: BLAST. Supporting evidence
 includes similarity to: 1 mRNA"
 /transcript_id="XM_210964.1"
 /db_xref="GI:27499426"
 /db_xref="InterimID:283295"
 STS 859321..859457
 /standard_name="D11S4708"
 /db_xref="UniSTS:21088"
 CDS complement(859657..859944)
 /gene="LOC283295"
 /codon_start=1
 /protein_id="XP_210964.1"
 /db_xref="GI:27499427"
 /db_xref="InterimID:283295"
 gene complement(860268..868789)
 /gene="KIAA0409"
 /db_xref="LocusID:23378"
 mRNA complement(join(865117..865458,865679..865775,
 865862..865968,866119..866248,866342..866795,
 867045..867408,868597..868774))
 /gene="KIAA0409"
 /product="KIAA0409 protein"
 /note="unclassified transcription discrepancy; Derived by
 automated computational analysis using gene prediction
 method: BestRefseq,BLAST. Supporting evidence includes
 similarity to: 1 mRNA"
 /transcript_id="NM_015324.1"
 /db_xref="GI:12758124"
 /db_xref="LocusID:23378"

STS 865126..865257
 /standard_name="WI-15843"
 /db_xref="UniSTS:3340"

STS 865136..865235
 /standard_name="G59726"
 /db_xref="UniSTS:137024"

STS 865146..865286
 /standard_name="RH47197"
 /db_xref="UniSTS:39346"

STS 865151..865287
 /standard_name="A007B37"
 /db_xref="UniSTS:16348"

CDS complement(join(865339..865458,865679..865775,
 865862..865968,866119..866248,866342..866795,
 867045..867408,868597..868695))
 /gene="KIAA0409"
 /note="unclassified translation discrepancy"
 /codon_start=1
 /evidence=not_experimental
 /product="KIAA0409 protein"
 /protein_id="NP_056139.1"
 /db_xref="GI:12758125"
 /db_xref="LocusID:23378"

STS 867136..867260
 /standard_name="WI-12713"
 /db_xref="UniSTS:10454"

gene 868947..876060
 /gene="ILK"
 /db_xref="LocusID:3611"
 /db_xref="MIM:602366"

mRNA join(868975..869015,869373..869553,873235..873400,
 873583..873678,873883..873979,874073..874156,
 874260..874345,874488..874597,874701..874828,
 874913..875034,875125..875224,875337..875467,
 875651..876055)
 /gene="ILK"
 /product="integrin-linked kinase"
 /note="unclassified transcription discrepancy; Derived by
 automated computational analysis using gene prediction
 method: BestRefseq,BLAST. Supporting evidence includes
 similarity to: 1 mRNA"
 /transcript_id="NM_004517.1"
 /db_xref="GI:4758605"
 /db_xref="LocusID:3611"
 /db_xref="MIM:602366"

CDS join(869465..869553,873235..873400,873583..873678,
 873883..873979,874073..874156,874260..874345,
 874488..874597,874701..874828,874913..875034,
 875125..875224,875337..875467,875651..875800)
 /gene="ILK"
 /function="protein serine/threonine kinase"
 /codon_start=1
 /product="integrin-linked kinase"
 /protein_id="NP_004508.1"
 /db_xref="GI:4758606"
 /db_xref="LocusID:3611"
 /db_xref="MIM:602366"

gene complement(871489..877403)
 /gene="TAF10"
 /db_xref="LocusID:6881"

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      /db_xref="MIM:600475"
STS      872508..872782
      /gene="ILK"
      /standard_name="WI-22555"
      /db_xref="UniSTS:5777"
      873528..873781
      /gene="ILK"
      /standard_name="RH12375"
      /db_xref="UniSTS:23970"
      875771..875992
      /gene="ILK"
      /standard_name="A002C40"
      /db_xref="UniSTS:5081"
mRNA      complement(join(876031..876200,876378..876492,
      876577..876641,876853..877007,877147..877403))
      /gene="TAF10"
      /product="TAF10 RNA polymerase II, TATA box binding
      protein (TBP)-associated factor, 30kDa"
      /note="Derived by automated computational analysis using
      gene prediction method: BestRefseq,BLAST. Supporting
      evidence includes similarity to: 1 mRNA"
      /transcript_id="NM_006284.2"
      /db_xref="GI:21166374"
      /db_xref="LocusID:6881"
      /db_xref="MIM:600475"
CDS      complement(join(876111..876200,876378..876492,
      876577..876641,876853..877007,877147..877378))
      /gene="TAF10"
      /note="TATA box binding protein (TBP)-associated factor,
      RNA polymerase II; TAF10 RNA polymerase II, TATA box
      binding protein (TBP)-associated factor, 30 kD; TATA box
      binding protein (TBP)-associated factor, RNA polymerase
      II, H, 30kD; transcription initiation factor TFIID 30 kD
      subunit"
      /codon_start=1
      /product="TBP-related factor 10"
      /protein_id="NP_006275.1"
      /db_xref="GI:5454106"
      /db_xref="LocusID:6881"
      /db_xref="MIM:600475"
STS      876607..876733
      /standard_name="RH70892"
      /db_xref="UniSTS:35021"
gene      complement(877958..884618)
      /gene="CLN2"
      /db_xref="LocusID:1200"
      /db_xref="MIM:204500"
mRNA      complement(join(877958..879875,880055..880180,
      880360..880518,880631..880751,881194..881263,
      881504..881692,881849..882047,882163..882341,
      882489..882616,882815..882965,883965..884104,
      884385..884456,884573..884618))
      /gene="CLN2"
      /product="ceroid-lipofuscinosis, neuronal 2, late
      infantile (Jansky-Bielschowsky disease)"
      /note="unclassified transcription discrepancy; Derived by
      automated computational analysis using gene prediction
      method: BestRefseq,BLAST. Supporting evidence includes
      similarity to: 1 mRNA"
      /transcript_id="NM_000391.2"

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/db_xref="GI:5597012"
/db_xref="LocusID:1200"
/db_xref="MIM:204500"
STS      877967..878092
         /standard_name="WI-11808"
         /db_xref="UniSTS:12935"
STS      879026..879140
         /standard_name="RH36325"
         /db_xref="UniSTS:18215"
CDS      complement(join(879735..879875,880055..880180,
880360..880518,880631..880751,881194..881263,
881504..881692,881849..882047,882163..882341,
882489..882616,882815..882965,883965..884104,
884385..884456,884573..884589))
         /gene="CLN2"
         /note="deficient in late-infantile neuronal ceroid
lipofuscinosis; unclassified translation discrepancy"
         /codon_start=1
         /product="ceroid-lipofuscinosis, neuronal 2, late
infantile (Jansky-Bielschowsky disease)"
         /protein_id="NP_000382.3"
         /db_xref="GI:5729770"
         /db_xref="LocusID:1200"
         /db_xref="MIM:204500"
STS      884275..884387
         /standard_name="D11S3007"
         /db_xref="UniSTS:152113"
gene     complement(886517..921034)
         /gene="PCDH16"
         /db_xref="LocusID:8642"
         /db_xref="MIM:603057"
mRNA     complement(join(886517..889580,889920..890058,
890388..890671,890787..890917,891110..891264,
891359..891570,891742..891855,891979..892857,
893811..894020,894642..894767,894862..895101,
895189..896053,896243..896400,896501..896597,
896806..896999,897221..898246,898602..898838,
898979..899210,899308..899496,905008..906924,
920754..920815))
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         /product="protocadherin 16 dachsous-like (Drosophila)"
         /note="unclassified transcription discrepancy; Derived by
automated computational analysis using gene prediction
method: BestRefseq,BLAST. Supporting evidence includes
similarity to: 1 mRNA"
         /transcript_id="NM_003737.1"
         /db_xref="GI:16933556"
         /db_xref="LocusID:8642"
         /db_xref="MIM:603057"
STS      886610..886776
         /standard_name="RH94204"
         /db_xref="UniSTS:88555"
CDS      complement(join(886969..889580,889920..890058,
890388..890671,890787..890917,891110..891264,
891359..891570,891742..891855,891979..892857,
893811..894020,894642..894767,894862..895101,
895189..896053,896243..896400,896501..896597,
896806..896999,897221..898246,898602..898838,
898979..899210,899308..899496,905008..906804))
         /gene="PCDH16"

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/note="unclassified translation discrepancy; protocadherin
16; fibroblast cadherin FIB1; fibroblast cadherin 1;
dachsaus homologue; cadherin related 25, dachsaus
(Drosophila) homolog"
/codon_start=1
/product="protocadherin 16 precursor"
/protein_id="NP_003728.1"
/db_xref="GI:16933557"
/db_xref="LocusID:8642"
/db_xref="MIM:603057"
STS      899445..899663
          /standard_name="SHGC-141500"
          /db_xref="UniSTS:182384"
STS      929631..929964
          /standard_name="RH119121"
          /db_xref="UniSTS:139013"
STS      945961..946201
          /standard_name="STS-AA039615"
          /db_xref="UniSTS:76931"
STS      946151..946322
          /standard_name="RH98881"
          /db_xref="UniSTS:90197"
gene      complement(946344..948534)
          /gene="MRPL17"
          /db_xref="LocusID:63875"
mRNA      complement(join(946840..947593,947938..948006,
948314..948534))
          /gene="MRPL17"
          /product="mitochondrial ribosomal protein L17"
          /note="Derived by automated computational analysis using
gene prediction method: BestRefseq,BLAST. Supporting
evidence includes similarity to: 2 mRNAs"
          /transcript_id="NM_022061.2"
          /db_xref="GI:27477130"
          /db_xref="LocusID:63875"
STS      947160..947309
          /standard_name="SGC33125"
          /db_xref="UniSTS:44831"
STS      947182..947334
          /standard_name="RH41797"
          /db_xref="UniSTS:7445"
CDS      complement(join(947309..947593,947938..948006,
948314..948487))
          /gene="MRPL17"
          /note="LYST-interacting protein LIP2"
          /codon_start=1
          /product="mitochondrial ribosomal protein L17"
          /protein_id="NP_071344.1"
          /db_xref="GI:11596859"
          /db_xref="LocusID:63875"
STS      947312..947496
          /standard_name="STS-T56255"
          /db_xref="UniSTS:5803"
STS      951373..951501
          /standard_name="SGC30555"
          /db_xref="UniSTS:62906"
STS      971066..971225
          /standard_name="WI-3891"
          /db_xref="UniSTS:76898"
STS      973547..973821

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/standard_name="SHGC-132044"
/db_xref="UniSTS:173888"
STS 973688..973837
/standard_name="SHGC-1124"
/db_xref="UniSTS:11419"
gene complement(978343..981721)
/ gene="FLJ13373"
/db_xref="LocusID:80073"
mRNA complement(979531..981655)
/ gene="FLJ13373"
/product="hypothetical protein FLJ13373"
/note="unclassified transcription discrepancy; Derived by
automated computational analysis using gene prediction
method: BestRefseq,BLAST. Supporting evidence includes
similarity to: 1. mRNA"
/transcript_id="NM_025006.1"
/db_xref="GI:13376522"
/db_xref="LocusID:80073"
CDS complement(979802..981190)
/ gene="FLJ13373"
/note="unclassified translation discrepancy"
/codon_start=1
/evidence=not_experimental
/product="hypothetical protein FLJ13373"
/protein_id="NP_079282.1"
/db_xref="GI:13376523"
/db_xref="LocusID:80073"
STS 986433..986624
/standard_name="RH120124"
/db_xref="UniSTS:132329"
STS 1003372..1003669
/standard_name="SHGC-84480"
/db_xref="UniSTS:102832"
STS 1005382..1005702
/standard_name="SHGC-111926"
/db_xref="UniSTS:182361"
gene complement(1008603..1011650)
/ gene="LOC283296"
/db_xref="InterimID:283296"
mRNA complement(1008603..1011650)
/ gene="LOC283296"
/product="LOC283296"
/note="Derived by automated computational analysis using
gene prediction method: BLAST. Supporting evidence
includes similarity to: 1 mRNA"
/transcript_id="XM_210966.1"
/db_xref="GI:27499428"
/db_xref="InterimID:283296"
CDS complement(1010888..1011364)
/ gene="LOC283296"
/codon_start=1
/protein_id="XP_210966.1"
/db_xref="GI:27499429"
/db_xref="InterimID:283296"
gene 1014396..1015224
/ gene="LOC338754"
/db_xref="InterimID:338754"
mRNA join(1014396..1014536,1014937..1015224)
/ gene="LOC338754"
/product="similar to hypothetical protein FLJ13373 [Homo

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sapiens]"
/note="Derived by automated computational analysis using
gene prediction method: GenomeScan."
/transcript_id="XM_291979.1"
/db_xref="GI:29746578"
/db_xref="InterimID:338754"
CDS
join(1014396..1014536,1014937..1015224)
/gene="LOC338754"
/codon_start=1
/protein_id="XP_291979.1"
/db_xref="GI:29746579"
/db_xref="InterimID:338754"
STS
1015393..1015518
/standard_name="D11S2706"
/db_xref="UniSTS:151929"
gene
complement(1033198..1034148)
/gene="LOC338755"
/db_xref="InterimID:338755"
mRNA
complement(1033198..1034148)
/gene="LOC338755"
/product="similar to Olfactory receptor 2AG1 (HT3)"
/note="Derived by automated computational analysis using
gene prediction method: GenomeScan."
/transcript_id="XM_291980.1"
/db_xref="GI:29746580"
/db_xref="InterimID:338755"
CDS
complement(1033198..1034148)
/gene="LOC338755"
/codon_start=1
/protein_id="XP_291980.1"
/db_xref="GI:29746581"
/db_xref="InterimID:338755"
misc_feature
1034664..1208274
/standard_name="RP11-560B16"
/note="FISH-mapped clone"
gene
1050199..1051149
/gene="LOC144125"
/db_xref="InterimID:144125"
mRNA
1050199..1051149
/gene="LOC144125"
/product="similar to Olfactory receptor 2AG1 (HT3)"
/note="Derived by automated computational analysis using
gene prediction method: GenomeScan."
/transcript_id="XM_090203.1"
/db_xref="GI:18605333"
/db_xref="InterimID:144125"
CDS
1050199..1051149
/gene="LOC144125"
/codon_start=1
/protein_id="XP_090203.1"
/db_xref="GI:18605334"
/db_xref="InterimID:144125"
gene
complement(1059885..1060868)
/gene="OR6A1"
/db_xref="LocusID:8590"
mRNA
complement(1059885..1060868)
/gene="OR6A1"
/product="olfactory receptor, family 6, subfamily A,
member 1"
/note="unclassified transcription discrepancy; Derived by

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automated computational analysis using gene prediction
 method: BestRefseq, BLAST. Supporting evidence includes
 similarity to: 1 mRNA
 /transcript_id="NM_003696.1"
 /db_xref="GI:4505520"
 /db_xref="LocusID:8590"
 CDS complement(1059885..1060868)
 /gene="OR6A1"
 /note="unclassified translation discrepancy"
 /codon_start=1
 /product="olfactory receptor, family 6, subfamily A,
 member 1"
 /protein_id="NP_003687.1"
 /db_xref="GI:4505521"
 /db_xref="LocusID:8590"
 gene 1110839..1111792
 /gene="LOC144124"
 /db_xref="InterimID:144124"
 mRNA 1110839..1111792
 /gene="LOC144124"
 /product="similar to Olfactory receptor 10A5 (HP3)
 (Olfactory receptor-like protein JCG6)"
 /note="Derived by automated computational analysis using
 gene prediction method: BLAST, GenomeScan. Supporting
 evidence includes similarity to: 1 mRNA"
 /transcript_id="XM_084745.1"
 /db_xref="GI:18605330"
 /db_xref="InterimID:144124"
 CDS 1110839..1111792
 /gene="LOC144124"
 /codon_start=1
 /protein_id="XP_084745.1"
 /db_xref="GI:18605331"
 /db_xref="InterimID:144124"
 gene 1128452..1135822
 /gene="LOC341276"
 /db_xref="InterimID:341276"
 mRNA join(1128452..1128507,1134847..1135822)
 /gene="LOC341276"
 /product="similar to hP4 olfactory receptor [Homo
 sapiens]"
 /note="Derived by automated computational analysis using
 gene prediction method: GenomeScan."
 /transcript_id="XM_291981.1"
 /db_xref="GI:29746586"
 /db_xref="InterimID:341276"
 CDS join(1128452..1128507,1134847..1135822)
 /gene="LOC341276"
 /codon_start=1
 /protein_id="XP_291981.1"
 /db_xref="GI:29746587"
 /db_xref="InterimID:341276"
 STS 1133437..1133561
 /gene="LOC341276"
 /standard_name="D11S3183"
 /db_xref="UniSTS:152429"
 gene 1141804..1142751
 /gene="LOC283297"
 /db_xref="InterimID:283297"
 mRNA 1141804..1142751

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/ gene="LOC283297"
/ product="similar to Olfactory receptor 10A4 (HP2)
(Olfactory receptor-like protein JCG5)"
/ note="Derived by automated computational analysis using
gene prediction method: BLAST, GenomeScan. Supporting
evidence includes similarity to: 1 mRNA"
/ transcript_id="XM_208604.1"
/ db_xref="GI:27499430"
/ db_xref="InterimID:283297"
CDS
1141804..1142751
/ gene="LOC283297"
/ codon_start=1
/ protein_id="XP_208604.1"
/ db_xref="GI:27499431"
/ db_xref="InterimID:283297"
gene
complement(1156730..1157656)
/ gene="LOC120776"
/ db_xref="InterimID:120776"
mRNA
complement(1156730..1157656)
/ gene="LOC120776"
/ product="similar to Olfactory receptor 2D2 (Olfactory
receptor 11-610) (OR11-610) (HB2)"
/ note="Derived by automated computational analysis using
gene prediction method: GenomeScan."
/ transcript_id="XM_062286.2"
/ db_xref="GI:18605326"
/ db_xref="InterimID:120776"
CDS
complement(1156730..1157656)
/ gene="LOC120776"
/ codon_start=1
/ protein_id="XP_062286.2"
/ db_xref="GI:18605327"
/ db_xref="InterimID:120776"
gene
1186206..1187150
/ gene="LOC120775"
/ db_xref="InterimID:120775"
mRNA
1186206..1187150
/ gene="LOC120775"
/ product="similar to olfactory receptor MOR260-2 [Mus
musculus]"
/ note="Derived by automated computational analysis using
gene prediction method: GenomeScan."
/ transcript_id="XM_062285.1"
/ db_xref="GI:17461456"
/ db_xref="InterimID:120775"
CDS
1186206..1187150
/ gene="LOC120775"
/ codon_start=1
/ protein_id="XP_062285.1"
/ db_xref="GI:17461457"
/ db_xref="InterimID:120775"
gene
1191579..1253643
/ gene="ZNF215"
/ db_xref="LocusID:7762"
/ db_xref="MIM:605016"
mRNA
join(1191579..1191841,1192818..1192963,1197250..1197828,
1206727..1206809,1208239..1208371,1208702..1208797,
1220846..1222993)
/ gene="ZNF215"
/ product="zinc finger protein 215"

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/note="unclassified transcription discrepancy; Derived by
automated computational analysis using gene prediction
method: BestRefseq,BLAST. Supporting evidence includes
similarity to: 3 mRNAs"
/transcript_id="NM_013250.1"
/db_xref="GI:7019582"
/db_xref="LocusID:7762"
/db_xref="MIM:605016"
STS 1194876..1194999
/gene="ZNF215"
/standard_name="RH65576"
/db_xref="UniSTS:45472"
CDS join(1197429..1197828,1206727..1206809,1208239..1208371,
1208702..1208797,1220846..1221687)
/gene="ZNF215"
/note="unclassified translation discrepancy"
/codon_start=1
/product="zinc finger protein 215"
/protein_id="NP_037382.1"
/db_xref="GI:7019583"
/db_xref="LocusID:7762"
/db_xref="MIM:605016"
STS 1222751..1222937
/gene="ZNF215"
/standard_name="RH98892"
/db_xref="UniSTS:89130"
STS 1226896..1227009
/gene="ZNF215"
/standard_name="G17601"
/db_xref="UniSTS:42468"
misc_feature 1228270..1423366
/standard_name="RP11-715M10"
/note="FISH-mapped clone"
gene complement(1264474..1285503)
/gene="ZNF214"
/db_xref="LocusID:7761"
/db_xref="MIM:605015"
mRNA complement(join(1264474..1266711,1267865..1268011,
1285229..1285466))
/gene="ZNF214"
/product="zinc finger protein 214"
/note="unclassified transcription discrepancy; Derived by
automated computational analysis using gene prediction
method: BestRefseq,BLAST. Supporting evidence includes
similarity to: 1 mRNA"
/transcript_id="NM_013249.1"
/db_xref="GI:7019580"
/db_xref="LocusID:7761"
/db_xref="MIM:605015"
CDS complement(join(1265018..1266711,1267865..1267991))
/gene="ZNF214"
/note="unclassified translation discrepancy"
/codon_start=1
/product="zinc finger protein 214"
/protein_id="NP_037381.1"
/db_xref="GI:7019581"
/db_xref="LocusID:7761"
/db_xref="MIM:605015"
STS 1279481..1279725
/standard_name="D11S1098"

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gene      /db_xref="UniSTS:2653"
          1303743..1336464
          /gene="NALP14"
          /db_xref="LocusID:338323"
mRNA      join(1303743..1304031,1304870..1304941,1307544..1309140,
          1311824..1311988,1314827..1314994,1322833..1323003,
          1323436..1323606,1325050..1325220,1327489..1327659,
          1335442..1335612,1336329..1336464)
          /gene="NALP14"
          /product="NALP14"
          /note="Derived by automated computational analysis using
          gene prediction method: BLAST. Supporting evidence
          includes similarity to: 1 mRNA"
          /transcript_id="NM_176822.1"
          /db_xref="GI:28827812"
          /db_xref="LocusID:338323"
CDS       join(1303743..1304031,1304870..1304941,1307544..1309140,
          1311824..1311988,1314827..1314994,1322833..1323003,
          1323436..1323606,1325050..1325220,1327489..1327659,
          1335442..1335612,1336329..1336464)
          /gene="NALP14"
          /note="member of the NALP protein family involved in
          inflammation; contains NACHT, LRR and PYD domains"
          /codon_start=1
          /product="NALP14"
          /protein_id="NP_789792.1"
          /db_xref="GI:28827813"
          /db_xref="LocusID:338323"
gene      1354208..1355814
          /gene="HNRNPG-T"
          /db_xref="LocusID:27288"
          /db_xref="MIM:605444"
mRNA      1354208..1355814
          /gene="HNRNPG-T"
          /product="testes-specific heterogenous nuclear
          ribonucleoprotein G-T"
          /note="unclassified transcription discrepancy; Derived by
          automated computational analysis using gene prediction
          method: BestRefseq,BLAST. Supporting evidence includes
          similarity to: 3 mRNAs"
          /transcript_id="NM_014469.2"
          /db_xref="GI:8850216"
          /db_xref="LocusID:27288"
          /db_xref="MIM:605444"
CDS       1354277..1355455
          /gene="HNRNPG-T"
          /note="unclassified translation discrepancy"
          /codon_start=1
          /product="testes-specific heterogenous nuclear
          ribonucleoprotein G-T"
          /protein_id="NP_055284.2"
          /db_xref="GI:8850217"
          /db_xref="LocusID:27288"
          /db_xref="MIM:605444"
STS       1355315..1355478
          /gene="HNRNPG-T"
          /standard_name="RH104373"
          /db_xref="UniSTS:98698"
STS       1409450..1409762
          /standard_name="SHGC-84693"

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STS      /db_xref="UniSTS:104092"
1421445..1421588
/standard_name="D11S2672"
/ db_xref="UniSTS:151898"
STS      1463253..1463544
/standard_name="D11S3249"
/ db_xref="UniSTS:152494"
STS      1484763..1485097
/standard_name="SHGC-142695"
/ db_xref="UniSTS:171597"
gene     1503934..1735188
/ gene="LOC143425"
/ db_xref="LocusID:143425"
mRNA     join(1517343..1517487,1568195..1568546,1578551..1579097,
1681198..1681318,1683113..1683284,1685662..1685791)
/ gene="LOC143425"
/product="similar to synaptotagmin V"
/ note="unclassified transcription discrepancy; Derived by
automated computational analysis using gene prediction
method: BestRefseq,BLAST. Supporting evidence includes
similarity to: 1 mRNA"
/transcript_id="NM_175733.1"
/ db_xref="GI:28376626"
/ db_xref="LocusID:143425"
CDS      join(1517343..1517487,1568195..1568546,1578551..1579097,
1681198..1681318,1683113..1683284,1685662..1685791)
/ gene="LOC143425"
/ note="unclassified translation discrepancy"
/ codon_start=1
/product="similar to synaptotagmin V"
/ protein_id="NP_783860.1"
/ db_xref="GI:28376627"
/ db_xref="LocusID:143425"
STS      1535937..1536135
/ gene="LOC143425"
/ standard_name="D11S1331"
/ db_xref="UniSTS:50340"
misc_feature 1535944..1536075
/ gene="LOC143425"
/ standard_name="RP11-205015"
/ note="FISH-mapped clone"
STS      1535944..1536075
/ gene="LOC143425"
/ standard_name="D11S1331"
/ db_xref="UniSTS:30804"
STS      1544996..1545200
/ gene="LOC143425"
/ standard_name="G49572"
/ db_xref="UniSTS:109241"
STS      1565296..1565624
/ gene="LOC143425"
/ standard_name="D11S3263"
/ db_xref="UniSTS:152506"
STS      1580983..1581276
/ gene="LOC143425"
/ standard_name="SHGC-147933"
/ db_xref="UniSTS:176105"
STS      1685400..1685512
/ gene="LOC143425"
/ standard_name="G49571"

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STS      /db_xref="UniSTS:109240"
1731110..1731360
/gene="LOC143425"
/standard_name="G17607"
STS      /db_xref="UniSTS:66698"
1732056..1732199
/gene="LOC143425"
/standard_name="D11S690"
STS      /db_xref="UniSTS:148165"
1732595..1732750
/gene="LOC143425"
/standard_name="A006P43"
STS      /db_xref="UniSTS:56377"
1733936..1734063
/gene="LOC143425"
/standard_name="RH12015"
STS      /db_xref="UniSTS:23147"
1733968..1734112
/gene="LOC143425"
/standard_name="A005E31"
STS      /db_xref="UniSTS:52157"
1748648..1748941
/standard_name="SHGC-153704"
/db_xref="UniSTS:177894"
gene      1750698..1776061
/gene="LOC283298"
/db_xref="InterimID:283298"
mRNA      join(1750698..1751160,1753283..1753571,1774554..1776061)
/gene="LOC283298"
/product="similar to hypothetical protein 6720478C22 [Mus
musculus]"
/note="Derived by automated computational analysis using
gene prediction method: BLAST. Supporting evidence
includes similarity to: 1 mRNA"
/transcript_id="XM_208606.1"
/db_xref="GI:27499432"
/db_xref="InterimID:283298"
CDS      join(1751032..1751160,1753283..1753571,1774554..1775344)
/gene="LOC283298"
/codon_start=1
/protein_id="XP_208606.1"
/db_xref="GI:27499433"
/db_xref="InterimID:283298"
STS      1775780..1775967
/gene="LOC283298"
/standard_name="RH66484"
/db_xref="UniSTS:56766"
STS      1776058..1776343
/standard_name="G62644"
/db_xref="UniSTS:139624"
gene      1778942..1918921
/gene="PPFIBP2"
/db_xref="LocusID:8495"
/db_xref="MIM:603142"
mRNA      join(1778942..1779277,1814596..1814695,1830709..1830923,
1858288..1858380,1862716..1862829,1875447..1875578,
1886091..1886183,1890933..1891047,1893441..1893502,
1894615..1894690,1896081..1896184,1898023..1898090,
1899651..1899708,1900708..1900749,1904888..1905026,
1906635..1906776,1907454..1907582,1913543..1913693,

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1913956..1914067,1914303..1914391,1914688..1914810,
1915996..1916121,1916812..1917000,1918180..1918914)
/gene="PPFIBP2"
/product="PTPRF interacting protein, binding protein 2
(liprin beta 2)"
/note="Derived by automated computational analysis using
gene prediction method: BLAST. Supporting evidence
includes similarity to: 5 mRNAs"
/transcript_id="XM_084578.6"
/db_xref="GI:27499434"
/db_xref="LocusID:8495"
/db_xref="MIM:603142"
CDS
join(1814632..1814695,1830709..1830923,1858288..1858380,
1862716..1862829,1875447..1875578,1886091..1886183,
1890933..1891047,1893441..1893502,1894615..1894690,
1896081..1896184,1898023..1898090,1899651..1899708,
1900708..1900749,1904888..1905026,1906635..1906776,
1907454..1907582,1913543..1913693,1913956..1914067,
1914303..1914391,1914688..1914810,1915996..1916121,
1916812..1917000,1918180..1918374)
/gene="PPFIBP2"
/codon_start=1
/protein_id="XP_084578.4"
/db_xref="GI:20561108"
/db_xref="LocusID:8495"
/db_xref="MIM:603142"
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1825408..1825712
/gene="PPFIBP2"
/standard_name="SHGC-82882"
/db_xref="UniSTS:104790"
STS
1825597..1825874
/gene="PPFIBP2"
/standard_name="SHGC-78819"
/db_xref="UniSTS:100821"
STS
1838829..1839104
/gene="PPFIBP2"
/standard_name="RH120212"
/db_xref="UniSTS:133205"
STS
1839513..1839733
/gene="PPFIBP2"
/standard_name="SHGC-112441"
/db_xref="UniSTS:182376"
STS
1852665..1852946
/gene="PPFIBP2"
/standard_name="SHGC-83011"
/db_xref="UniSTS:101281"
STS
1869059..1869256
/gene="PPFIBP2"
/standard_name="RH45476"
/db_xref="UniSTS:70768"
STS
1869144..1869412
/gene="PPFIBP2"
/standard_name="D11S1208"
/db_xref="UniSTS:10190"
STS
1887270..1887365
/gene="PPFIBP2"
/standard_name="SHGC-14320"
/db_xref="UniSTS:25229"
STS
1915876..1916177
/gene="PPFIBP2"

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/standard_name="SHGC-154807"
/db_xref="UniSTS:178167"
STS 1916847..1916972
/gene="PPFIBP2"
/standard_name="G54152"
/db_xref="UniSTS:109389"
STS 1918662..1918896
/gene="PPFIBP2"
/standard_name="A004U29"
/db_xref="UniSTS:50995"
gene complement(1930261..1942376)
/gene="CYB5R2"
/db_xref="LocusID:51700"
mRNA complement(join(1930261..1930702,1931607..1931706,
1932884..1932969,1933634..1933717,1934361..1934490,
1934781..1934887,1937607..1937679,1937904..1938047,
1938575..1938657))
/gene="CYB5R2"
/product="cytochrome b5 reductase b5R.2"
/note="unclassified transcription discrepancy; Derived by
automated computational analysis using gene prediction
method: BestRefseq,BLAST. Supporting evidence includes
similarity to: 1 mRNA"
/transcript_id="NM_016229.1"
/db_xref="GI:7706442"
/db_xref="LocusID:51700"
STS 1930270..1930470
/standard_name="STS-N90805"
/db_xref="UniSTS:79630"
CDS complement(join(1930532..1930702,1931607..1931706,
1932884..1932969,1933634..1933717,1934361..1934490,
1934781..1934887,1937607..1937679,1937904..1937981))
/gene="CYB5R2"
/note="unclassified translation discrepancy"
/codon_start=1
/product="cytochrome b5 reductase b5R.2"
/protein_id="NP_057313.1"
/db_xref="GI:7706443"
/db_xref="LocusID:51700"
STS 1932139..1932280
/standard_name="D11S4068"
/db_xref="UniSTS:154198"
STS 1932191..1932354
/standard_name="RH15972"
/db_xref="UniSTS:70824"
STS 1952358..1952598
/standard_name="D11S1996"
/db_xref="UniSTS:17642"
gene complement(1955111..1971866)
/gene="LOC341277"
/db_xref="InterimID:341277"
mRNA complement(join(1955111..1955169,1956425..1956556,
1957058..1957139,1960214..1960344,1960726..1960808,
1961774..1962061,1962181..1962271,1964222..1964245,
1965768..1965957,1966796..1966947,1967188..1967283,
1967629..1967801,1969170..1969261,1970037..1970146,
1971779..1971866))
/gene="LOC341277"
/product="similar to hypothetical protein 9230106D23 [Mus
musculus]"

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/note="Derived by automated computational analysis using
gene prediction method: GenomeScan."
/transcript_id="XM_291982.1"
/db_xref="GI:29746588"
/db_xref="InterimID:341277"
CDS complement(join(1955111..1955169,1956425..1956556,
1957058..1957139,1960214..1960344,1960726..1960808,
1961774..1962061,1962181..1962271,1964222..1964245,
1965768..1965957,1966796..1966947,1967188..1967283,
1967629..1967801,1969170..1969261,1970037..1970146,
1971779..1971866))
/gene="LOC341277"
/codon_start=1
/protein_id="XP_291982.1"
/db_xref="GI:29746589"
/db_xref="InterimID:341277"
misc_feature 1974740..2100479
/standard_name="RP11-25D22"
/note="FISH-mapped clone"
misc_feature 1982544..2156690
/standard_name="RP11-399N15"
/note="FISH-mapped clone"
gene 1993995..1994855
/gene="LOC120061"
/db_xref="InterimID:120061"
mRNA 1993995..1994855
/gene="LOC120061"
/product="similar to seven transmembrane helix receptor
[Homo sapiens]"
/note="Derived by automated computational analysis using
gene prediction method: GenomeScan."
/transcript_id="XM_061838.2"
/db_xref="GI:22061586"
/db_xref="InterimID:120061"
CDS 1993995..1994855
/gene="LOC120061"
/codon_start=1
/protein_id="XP_061838.2"
/db_xref="GI:22061587"
/db_xref="InterimID:120061"
gene 2011452..2012374
/gene="LOC120062"
/db_xref="InterimID:120062"
mRNA join(2011452..2011768,2011783..2012374)
/gene="LOC120062"
/product="similar to olfactory receptor MOR204-2 [Mus
musculus]"
/note="Derived by automated computational analysis using
gene prediction method: GenomeScan."
/transcript_id="XM_061839.2"
/db_xref="GI:22061590"
/db_xref="InterimID:120062"
CDS join(2011452..2011768,2011783..2012374)
/gene="LOC120062"
/codon_start=1
/protein_id="XP_061839.2"
/db_xref="GI:22061591"
/db_xref="InterimID:120062"
STS 2018101..2018226
/standard_name="D11S3672"

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gene      /db_xref="UniSTS:152906"
          complement(2038353..2039277)
          /gene="LOC341278"
mRNA      /db_xref="InterimID:341278"
          complement(join(2038353..2038972,2039061..2039277))
          /gene="LOC341278"
          /product="similar to olfactory receptor MOR204-11 [Mus
          musculus]"
          /note="Derived by automated computational analysis using
          gene prediction method: GenomeScan."
          /transcript_id="XM_291983.1"
          /db_xref="GI:29746590"
          /db_xref="InterimID:341278"
CDS       complement(join(2038353..2038972,2039061..2039277))
          /gene="LOC341278"
          /codon_start=1
          /protein_id="XP_291983.1"
          /db_xref="GI:29746591"
          /db_xref="InterimID:341278"
gene      2049160..2049870
          /gene="LOC120064"
          /db_xref="InterimID:120064"
mRNA      join(2049160..2049218,2049261..2049457,2049567..2049687,
          2049738..2049870)
          /gene="LOC120064"
          /product="similar to 60S ribosomal protein L7A (Surfeit
          locus protein 3)"
          /note="Derived by automated computational analysis using
          gene prediction method: GenomeScan."
          /transcript_id="XM_061841.1"
          /db_xref="GI:17472928"
          /db_xref="InterimID:120064"
CDS       join(2049160..2049218,2049261..2049457,2049567..2049687,
          2049738..2049870)
          /gene="LOC120064"
          /codon_start=1
          /protein_id="XP_061841.1"
          /db_xref="GI:17472929"
          /db_xref="InterimID:120064"
gene      complement(2061437..2062405)
          /gene="JCG3"
          /db_xref="LocusID:120065"
mRNA      complement(2061437..2062405)
          /gene="JCG3"
          /product="olfactory receptor-like protein JCG3"
          /note="Derived by automated computational analysis using
          gene prediction method: BestRefseq,BLAST. Supporting
          evidence includes similarity to: 3 mRNAs"
          /transcript_id="NM_153444.1"
          /db_xref="GI:23592221"
          /db_xref="LocusID:120065"
CDS       complement(2061437..2062405)
          /gene="JCG3"
          /codon_start=1
          /product="olfactory receptor-like protein JCG3"
          /protein_id="NP_703145.1"
          /db_xref="GI:23592222"
          /db_xref="LocusID:120065"
gene      complement(2090500..2091435)
          /gene="JCG1"

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mRNA
 /db_xref="LocusID:120066"
 complement(2090500..2091435)
 /gene="JCG1"
 /product="olfactory receptor-like protein JCG1"
 /note="Derived by automated computational analysis using
 gene prediction method: BestRefseq, BLAST. Supporting
 evidence includes similarity to: 2 mRNAs"
 /transcript_id="NM_153445.1"
 /db_xref="GI:23592229"
 /db_xref="LocusID:120066"
 CDS
 complement(2090500..2091435)
 /gene="JCG1"
 /codon_start=1
 /product="olfactory receptor-like protein JCG1"
 /protein_id="NP_703146.1"
 /db_xref="GI:23592230"
 /db_xref="LocusID:120066"
 STS
 2092558..2092877
 /standard_name="SHGC-149151"
 /db_xref="UniSTS:176832"
 misc_feature
 2100330..2100479
 /standard_name="RP11-799H15"
 /note="FISH-mapped clone"
 STS
 2100330..2100479
 /standard_name="SHGC-30914"
 /db_xref="UniSTS:34295"
 gene
 2114514..2115098
 /gene="OR5E1P"
 /pseudo
 /db_xref="LocusID:26343"
 gene
 complement(2116214..2171418)
 /gene="LOC283299"
 /db_xref="InterimID:283299"
 mRNA
 complement(join(2116214..2117787,2120346..2120426,
 2144470..2144546,2145058..2145222,2146552..2146612,
 2147419..2147536,2148323..2148396,2171066..2171418))
 /gene="LOC283299"
 /product="LOC283299"
 /note="Derived by automated computational analysis using
 gene prediction method: BLAST. Supporting evidence
 includes similarity to: 1 mRNA"
 /transcript_id="XM_210965.1"
 /db_xref="GI:27499435"
 /db_xref="InterimID:283299"
 CDS
 complement(2116906..2117328)
 /gene="LOC283299"
 /codon_start=1
 /protein_id="XP_210965.1"
 /db_xref="GI:27499436"
 /db_xref="InterimID:283299"
 misc_feature
 2145539..2281898
 /standard_name="RP11-21N2"
 /note="FISH-mapped clone"
 gene
 complement(2193181..2194125)
 /gene="LOC341279"
 /db_xref="InterimID:341279"
 mRNA
 complement(2193181..2194125)
 /gene="LOC341279"
 /product="similar to seven transmembrane helix receptor
 [Homo sapiens]"

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/Note="Derived by automated computational analysis using
gene prediction method: GenomeScan."
/transcript_id="XM_291985.1"
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complement(2193181..2194125)
/gene="LOC341279"
/codon_start=1
/protein_id="XP_291985.1"
/db_xref="GI:29746593"
/db_xref="InterimID:341279"
complement(2204039..2204983)
/gene="OR10A3"
/db_xref="LocusID:26496"
complement(2204039..2204983)
/gene="OR10A3"
/product="olfactory receptor, family 10, subfamily A,
member 3"
/Note="Derived by automated computational analysis using
gene prediction method: GenomeScan."
/transcript_id="XM_291986.1"
/db_xref="GI:29746594"
/db_xref="LocusID:26496"
complement(2204039..2204983)
/gene="OR10A3"
/codon_start=1
/protein_id="XP_291986.1"
/db_xref="GI:29746595"
/db_xref="LocusID:26496"
2213429..2213723
/standard_name="SHGC-142522"
/db_xref="UniSTS:171506"
complement(2225107..2228958)
/gene="NALP10"
/db_xref="LocusID:338322"
complement(join(2225107..2226785,2228670..2228958))
/gene="NALP10"
/product="NALP10"
/Note="Derived by automated computational analysis using
gene prediction method: BLAST. Supporting evidence
includes similarity to: 1 mRNA"
/transcript_id="NM_176821.1"
/db_xref="GI:28827806"
/db_xref="LocusID:338322"
complement(join(2225107..2226785,2228670..2228958))
/gene="NALP10"
/Note="member of the NALP protein family involved in
inflammation; contains NACHT and PYD domains; NALPs"
/codon_start=1
/product="NALP10"
/protein_id="NP_789791.1"
/db_xref="GI:28827807"
/db_xref="LocusID:338322"
2235714..2263623
/gene="EIF3S5"
/db_xref="LocusID:8665"
/db_xref="MIM:603914"
2236942..2237202
/gene="EIF3S5"
/standard_name="D11S2839"

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mRNA      /db_xref="UniSTS:152025"
          join(2252810..2253179,2257244..2257314,2257547..2257626,
          2258350..2258487,2259889..2259980,2260445..2260581,
          2260717..2260830,2261408..2261627)
          /gene="EIF3S5"
          /product="eukaryotic translation initiation factor 3,
          subunit 5 epsilon, 47kDa"
          /note="unclassified transcription discrepancy; Derived by
          automated computational analysis using gene prediction
          method: BestRefseq,BLAST. Supporting evidence includes
          similarity to: 1 mRNA"
          /transcript_id="NM_003754.1"
          /db_xref="GI:4503518"
          /db_xref="LocusID:8665"
          /db_xref="MIM:603914"
CDS        join(2252816..2253179,2257244..2257314,2257547..2257626,
          2258350..2258487,2259889..2259980,2260445..2260581,
          2260717..2260830,2261408..2261485)
          /gene="EIF3S5"
          /note="eukaryotic translation initiation factor 3, subunit
          5 (epsilon, 47kD)"
          /codon_start=1
          /product="eukaryotic translation initiation factor 3,
          subunit 5 epsilon, 47kDa"
          /protein_id="NP_003745.1"
          /db_xref="GI:4503519"
          /db_xref="LocusID:8665"
          /db_xref="MIM:603914"
STS        2259514..2259666
          /gene="EIF3S5"
          /standard_name="D11S1152"
          /db_xref="UniSTS:19122"
STS        2265903..2266014
          /standard_name="RH18331"
          /db_xref="UniSTS:81654"
STS        2267138..2267225
          /standard_name="STS-F03421"
          /db_xref="UniSTS:55985"
STS        2281505..2281813
          /standard_name="SHGC-78923"
          /db_xref="UniSTS:182491"
gene       2284729..2368411
          /gene="TUB"
          /db_xref="LocusID:7275"
          /db_xref="MIM:601197"
mRNA       join(2304096..2304491,2305108..2305155,2355073..2355124,
          2355532..2355694,2359509..2359652,2360961..2361128,
          2362148..2362269,2362691..2362888,2363177..2363289,
          2364221..2364338,2365966..2366064,2366289..2366460,
          2366949..2368411)
          /gene="TUB"
          /product="tubby homolog (mouse)"
          /note="unclassified transcription discrepancy; Derived by
          automated computational analysis using gene prediction
          method: BestRefseq,BLAST. Supporting evidence includes
          similarity to: 2 mRNAs"
          /transcript_id="NM_003320.2"
          /db_xref="GI:19923166"
          /db_xref="LocusID:7275"
          /db_xref="MIM:601197"

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CDS join(2304337..2304491,2305108..2305155,2355073..2355124,
 2355532..2355694,2359509..2359652,2360961..2361128,
 2362148..2362269,2362691..2362888,2363177..2363289,
 2364221..2364338,2365966..2366064,2366289..2366460,
 2366949..2367082)
 /gene="TUB"
 /function="unknown"
 /note="tubby (mouse) homolog"
 /codon_start=1
 /product="tubby homolog (mouse)"
 /protein_id="NP_003311.2"
 /db_xref="GI:19923167"
 /db_xref="LocusID:7275"
 /db_xref="MIM:601197"
 STS 2358483..2358682
 /gene="TUB"
 /standard_name="RH36564"
 /db_xref="UniSTS:55145"
 gene complement(2371564..2434486)
 /gene="FLJ11608"
 /db_xref="LocusID:79608"
 mRNA complement(join(2374412..2376600,2392120..2392265,
 2402839..2402932,2403733..2403808,2405428..2405654,
 2434327..2434483))
 /gene="FLJ11608"
 /product="hypothetical protein FLJ11608"
 /note="unclassified transcription discrepancy; Derived by
 automated computational analysis using gene prediction
 method: BestRefseq,BLAST. Supporting evidence includes
 similarity to: 1 mRNA"
 /transcript_id="NM_024557.2"
 /db_xref="GI:21362039"
 /db_xref="LocusID:79608"
 STS 2374425..2374555
 /standard_name="WI-14382"
 /db_xref="UniSTS:24731"
 CDS complement(join(2376161..2376600,2392120..2392265,
 2402839..2402932,2403733..2403808,2405428..2405654,
 2434327..2434450))
 /gene="FLJ11608"
 /note="unclassified translation discrepancy"
 /codon_start=1
 /evidence=not_experimental
 /product="hypothetical protein FLJ11608"
 /protein_id="NP_078833.2"
 /db_xref="GI:21362040"
 /db_xref="LocusID:79608"
 STS 2463789..2464120
 /standard_name="SHGC-148637"
 /db_xref="UniSTS:176517"
 STS 2478374..2478714
 /standard_name="D11S3436"
 /db_xref="UniSTS:152677"
 gene complement(2489771..2534177)
 /gene="LM01"
 /db_xref="LocusID:4004"
 /db_xref="MIM:186921"
 mRNA complement(join(2489771..2490182,2492436..2492561,
 2495752..2495965,2528799..2529320))
 /gene="LM01"

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/product="LIM domain only 1 (rhombotin 1)"
/note="unclassified transcription discrepancy; Derived by
automated computational analysis using gene prediction
method:~BestRefseq,BLAST. Supporting evidence includes
similarity to: 3 mRNAs"
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/db_xref="LocusID:4004"
/db_xref="MIM:186921"
STS      2489794..2489968
          /standard_name="D11S4594"
          /db_xref="UniSTS:29757"
STS      2489856..2490012
          /standard_name="LMO1"
          /db_xref="UniSTS:26133"
CDS      complement(join(2490077..2490182,2492436..2492561,
2495752..2495965,2528799..2528823))
          /gene="LMO1"
          /note="Lmol"
          /codon_start=1
          /product="LIM domain only 1"
          /protein_id="NP_002306.1"
          /db_xref="GI:4505005"
          /db_xref="LocusID:4004"
          /db_xref="MIM:186921"
STS      2578643..2578975
          /standard_name="SHGC-148827"
          /db_xref="UniSTS:176632"
STS      2597737..2597892
          /standard_name="G29013"
          /db_xref="UniSTS:10871"
STS      2613526..2613799
          /standard_name="D11S3261"
          /db_xref="UniSTS:152504"
misc_feature 2634677..2634828
          /standard_name="CTB-2P10"
          /note="FISH-mapped clone"
STS      2634677..2634828
          /standard_name="D11S932"
          /db_xref="UniSTS:67475"
STS      2636239..2636339
          /standard_name="D11S2704"
          /db_xref="UniSTS:151927"
STS      2652365..2652662
          /standard_name="SHGC-145524"
          /db_xref="UniSTS:174627"
gene      complement(2657332..2798958)
          /gene="STK33"
          /db_xref="LocusID:65975"
STS      2657354..2657528
          /standard_name="SGC44503"
          /db_xref="UniSTS:79706"
mRNA      complement(join(2657371..2658171,2678956..2679153,
2700955..2701040,2701488..2701600,2706139..2706214,
2718283..2718367,2720205..2720293,2722802..2722940,
2727266..2727370,2730170..2730283,2738624..2738737,
2740142..2741285))
          /gene="STK33"
          /product="serine/threonine kinase 33"
          /note="unclassified transcription discrepancy; Derived by

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automated computational analysis using gene prediction
method: BestRefseq,BLAST. Supporting evidence includes
similarity to: 1 mRNA"
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/db_xref="LocusID:65975"
STS      2657383..2657494
         /standard_name="SHGC-44503"
         /db_xref="UniSTS:25962"
STS      2657665..2657786
         /standard_name="RH92437"
         /db_xref="UniSTS:90136"
CDS      complement(join(2657971..2658171,2678956..2679153,
2700955..2701040,2701488..2701600,2706139..2706214,
2718283..2718367,2720205..2720293,2722802..2722940,
2727266..2727370,2730170..2730283,2738624..2738737,
2740142..2740366))
         /gene="STK33"
         /codon_start=1
         /product="serine/threonine kinase 33"
         /protein_id="NP_112168.1"
         /db_xref="GI:23943882"
         /db_xref="LocusID:65975"
STS      2742574..2742720
         /standard_name="D11S431"
         /db_xref="UniSTS:148537"
STS      2762937..2763250
         /standard_name="D11S3426"
         /db_xref="UniSTS:152667"
CONTIG   join(complement(AC131574.4:2930..166214),AC025016.8:1..74840,
complement(AC111177.15:1..165682),AC022762.8:54839..186604,
AC068733.12:8771..191656,AC084337.7:42081..112295,
AC009796.6:67320..192239,AC091564.12:45902..211735,
AC087280.11:44766..173611,AC090160.6:30193..170008,
complement(AC100875.3:1..75276),AC027804.7:42630..172272,
AC060799.6:15779..152164,complement(AC107884.15:1348..164472),
complement(AC104237.2:1..164732),AC021427.10:34710..174147,
AC044810.7:112096..194297,complement(AC124259.6:1..43031),
AC116456.12:43903..146502,complement(AC129895.5:55633..103080),
complement(AC091013.7:4558..223741),AC105357.7:1..167772)
//
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1: NT_009334[gi:15314816] This record was removed as a result of standard genome annotation processing. See the genome build documentation at <http://www.ncbi.nlm.nih.gov/genome/guide/build.html> for further information, or contact info@ncbi.nlm.nih.gov.

LOCUS NT_009334 5196829 bp DNA linear CON 27-AUG-2001
 DEFINITION Homo sapiens chromosome 11 working draft sequence segment.
 ACCESSION NT_009334
 VERSION NT_009334.5 GI:15314816
 KEYWORDS .
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 5196829)
 AUTHORS NCBI Annotation Project.
 TITLE Direct Submission
 JOURNAL Submitted (23-AUG-2001) National Center for Biotechnology
 Information, NIH, Bethesda, MD 20894, USA
 COMMENT GENOME ANNOTATION REFSEQ: NCBI contigs are derived from assembled
 genomic sequence data.
 Also see:
 Documentation of NCBI's Annotation Process

On Aug 27, 2001 this sequence version replaced gi:14774332.
 COMPLETENESS: not full length.

FEATURES Location/Qualifiers
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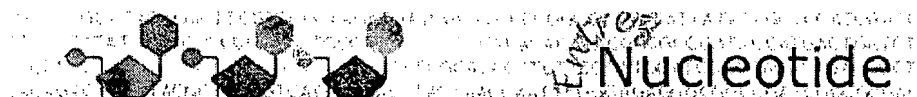
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☐ 1: NT_024766[gi:18585923] This record was removed as a result of standard genome annotation processing. See the genome build documentation at <http://www.ncbi.nlm.nih.gov/genome/guide/build.html> for further information, or contact info@ncbi.nlm.nih.gov.

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 DEFINITION Homo sapiens chromosome 16 working draft sequence segment.
 ACCESSION NT_024766
 VERSION NT_024766.5 GI:18585923
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 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 531499)
 AUTHORS NCBI Annotation Project.
 TITLE Direct Submission
 JOURNAL Submitted (06-FEB-2002) National Center for Biotechnology
 Information, NIH, Bethesda, MD 20894, USA
 COMMENT GENOME ANNOTATION REFSEQ: NCBI contigs are derived from assembled
 genomic sequence data.
 Also see:
 Documentation of NCBI's Annotation Process

On Feb 7, 2002 this sequence version replaced gi:14778846.
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gene            complement(98273..132250)
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                /note="Located on Accession NT_024766"
                /db_xref="LocusID:80011"
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STS 98352..98512
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          163139..163205,163936..164067,167764..167879,
          168304..168447,174374..174485,177743..177845,
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/ db_xref="UniSTS:14411"
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/ note="Located on Accession NT_024766"
/ db_xref="LocusID:23568"
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/db_xref="LocusID:51090"
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/product="plasmolipin"
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226702..226791,229921..230004,248354..248437,
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261731..261815,262314..262379,264522..264581,
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                /note="synonyms: TSC, NCCT; Located on Accession
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                /db_xref="LocusID:6559"
                /db_xref="MIM:600968"
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                414518..414624,415456..415596,416079..416190,
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                422302..422425,422906..423013,423328..423482,
                424394..424478,430872..431002,431196..431307,
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gene complement (397705..400324)

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/ db_xref="InterimID:146472"
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/ gene="LOC146472"
/ note="Located on Accession NT_024766"
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/ note="Derived by automated computational analysis using
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/ db_xref="LocusID:9688"
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/ product="KIAA0095 gene product"
/ note="unclassified transcription discrepancy; Derived by
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          /note="Located on Accession NT_024766"
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          /db_xref="InterimID:162128"
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☐ 1: NT_015360[gi:18585813] This record was removed as a result of standard genome annotation processing. See the genome build documentation at <http://www.ncbi.nlm.nih.gov/genome/guide/build.html> for further information, or contact info@ncbi.nlm.nih.gov.

LOCUS NT_015360 1074911 bp DNA linear CON 07-FEB-2002
 DEFINITION Homo sapiens chromosome 16 working draft sequence segment.
 ACCESSION NT_015360
 VERSION NT_015360.8 GI:18585813
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 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1074911)
 AUTHORS NCBI Annotation Project.
 TITLE Direct Submission
 JOURNAL Submitted (06-FEB-2002) National Center for Biotechnology
 Information, NIH, Bethesda, MD 20894, USA
 COMMENT GENOME ANNOTATION REFSEQ: NCBI contigs are derived from assembled
 genomic sequence data.
 Also see:
 Documentation of NCBI's Annotation Process

On Feb 7, 2002 this sequence version replaced gi:17487958.
 COMPLETENESS: not full length.

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          /db_xref="dbSNP:1218763"
variation 5080
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          /db_xref="dbSNP:1230946"
variation 12402
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          /db_xref="dbSNP:1149497"
variation 14162
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gene      complement(15469..28060)
          /gene="LOC162103"
          /note="Located on Accession NT_015360"
          /db_xref="InterimID:162103"
mRNA      complement(join(15469..15506,15982..16056,16195..16299,
          16442..16609,21681..21709,24619..24810,24992..25178,
          27958..28060))
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          /product="similar to cytochrome c oxidase subunit I"
          /note="Derived by automated computational analysis using
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          /transcript_id="XM_091357.1"
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      /note="unclassified transcription discrepancy; Derived by
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method: BLAST. Supporting evidence includes similarity to:
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      /db_xref="LocusID:54925"
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      /db_xref="UniSTS:25170"
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gene      complement(31080..48373)
      /gene="MGC4179"
      /note="Located on Accession NT_015360"
      /db_xref="LocusID:79229"
mRNA      complement(join(31080..31113,31861..32343,37410..37533,
37823..37917,41058..41223,44601..45153,48354..48373))
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      /note="unclassified transcription discrepancy; Derived by
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method: BLAST. Supporting evidence includes similarity to:
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      /db_xref="LocusID:79229"
STS      31263..31389
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variation 32101
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CDS      complement(join(83813..84927,88200..88326,90513..90545))
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gene          123007..137720
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              /note="Located on Accession NT_015360"
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                /note="Located on Accession NT_015360"
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                /product="similar to dJ475N16.3 (novel protein similar to
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                /note="Derived by automated computational analysis using
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variation	162471 /gene="LOC124208" /allele="T" /allele="A" /db_xref="dbSNP:1231091"
variation	166819 /gene="LOC124208" /allele="G" /allele="A" /db_xref="dbSNP:250470"
variation	167346 /gene="LOC124208" /allele="C" /allele="A" /db_xref="dbSNP:37846"
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variation	169841 /gene="LOC124208" /allele="T" /allele="C" /db_xref="dbSNP:190373"
variation	170393 /gene="LOC124208" /allele="T" /allele="C" /db_xref="dbSNP:2360762"
variation	175051 /allele="T" /allele="G" /db_xref="dbSNP:37842"
variation	175677

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              /db_xref="dbSNP:1963299"
STS          176977..177101
              /standard_name="SHGC-60769"
              /db_xref="UniSTS:33463"
gene         complement(177219..193992)
              /gene="LOC146435"
              /note="Located on Accession NT_015360"
              /db_xref="InterimID:146435"
mRNA         complement(join(177219..178603,178771..178881,
              182618..182744,183025..183116,183845..184040,
              190150..190582,193785..193992))
              /gene="LOC146435"
              /product="similar to unnamed protein product"
              /note="Derived by automated computational analysis using
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              includes similarity to: 1 mRNA"
              /transcript_id="XM_085465.1"
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              /db_xref="InterimID:146435"
STS          177267..177398
              /standard_name="RH45212"
              /db_xref="UniSTS:90620"
STS          177336..177609
              /standard_name="RH69709"
              /db_xref="UniSTS:27702"
STS          177338..177612
              /standard_name="SHGC-133103"
              /db_xref="UniSTS:171017"
STS          177437..177579
              /standard_name="SHGC-64870"
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CDS          complement(join(177924..178603,178771..178881,
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              /note="Located on Accession NT_015360"
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mRNA           join(194393..196690,205243..205294)
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                /note="unclassified transcription discrepancy; Derived by
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                method: BLAST. Supporting evidence includes similarity to:
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         /db_xref="UniSTS:84932"
variation 197622
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variation 199564
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variation 201175
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variation 201743
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         /db_xref="dbSNP:1149486"
variation 202694
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         /allele="G"
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         /db_xref="dbSNP:1052997"
gene      complement(204336..205570)
         /gene="LOC146436"
         /note="Located on Accession NT_015360"
         /db_xref="InterimID:146436"
mRNA      complement(join(204336..204531,205253..205570))
         /gene="LOC146436"
         /product="similar to FPM315"
         /note="Derived by automated computational analysis using
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         /transcript_id="XM_085469.1"
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gene      complement(204339..212266)
         /gene="ZNF263"
         /note="synonym: FPM315; Located on Accession NT_015360"
         /db_xref="LocusID:10127"
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 /db_xref="GI:5032240"
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STS 204492..204658
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 /db_xref="UniSTS:39552"
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 /db_xref="GI:18585767"
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STS 204528..204666
 /gene="LOC91151"
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 /db_xref="UniSTS:152425"

variation 204948
 /gene="LOC91151"
 /allele="G"
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 /db_xref="dbSNP:220380"

variation 205184
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variation 205185
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CDS complement(join(205235..206400,207223..207339,209644..209770,210039..210112,210554..210734,211588..211974))
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                /note="Located on Accession NT_015360"
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mRNA           complement(join(212827..213079,222078..222115))
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                /transcript_id="NM_003456.1"
                /db_xref="GI:4508014"
                /db_xref="LocusID:7755"
                /db_xref="MIM:603436"
STS           375288..375480
                /standard_name="STS-W93354"
                /db_xref="UniSTS:57067"
CDS           complement(join(375475..376544,376785..376895,
                379257..379377,379884..379975,380235..380355))
                /gene="ZNF205"
                /note="zinc finger type C2H2; contains KRAB domain; zinc
                finger protein 210"
                /codon_start=1
                /product="zinc finger protein 205"
                /protein_id="NP_003447.1"
                /db_xref="GI:4508015"
                /db_xref="LocusID:7755"
                /db_xref="MIM:603436"
variation      375613
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                /db_xref="dbSNP:12032"
variation      376965
                /allele="C"
                /allele="A"
                /db_xref="dbSNP:224181"
variation      377076
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                /db_xref="dbSNP:224180"
variation      377734
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                /db_xref="dbSNP:224179"
variation      379218
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                /allele="C"
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variation      379661
                /allele="C"
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variation      380121
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                /db_xref="dbSNP:2280951"
gene           380203..385342
                /gene="MGC3771"
                /note="synonym: MGC1912; Located on Accession NT_015360"
                /db_xref="LocusID:81854"
mRNA           join(380203..380835,380916..381008,384849..385342)
                /gene="MGC3771"
                /product="hypothetical protein MGC3771"
                /note="Derived by automated computational analysis using
                gene prediction method: BLAST. Supporting evidence
                includes similarity to: 2 mRNAs"
                /transcript_id="XM_036491.1"
                /db_xref="GI:14777842"
                /db_xref="LocusID:81854"
variation      380379
                /gene="MGC3771"
                /note="WARNING: map location ambiguous"
                /allele="T"
                /allele="C"
                /db_xref="dbSNP:909410"
variation      380753
                /gene="MGC3771"
                /note="WARNING: map location ambiguous"
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variation      381105
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                /note="WARNING: map location ambiguous"
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variation      381524
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                /db_xref="dbSNP:125772"
STS           382403..382729
                /gene="MGC3771"
                /standard_name="RH119820"
                /note="WARNING: map location ambiguous"
                /db_xref="UniSTS:133510"
variation      382666
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                /note="WARNING: map location ambiguous"
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                /allele="C"
                /db_xref="dbSNP:2280950"
gene           383314..385291
                /gene="LOC146438"
                /note="Located on Accession NT_015360"
                /db_xref="InterimID:146438"
mRNA           join(383314..383520,384849..385291)
                /gene="LOC146438"
                /product="similar to PRO2550"
                /note="Derived by automated computational analysis using

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gene prediction method: BLAST."
/transcript_id="XM_085464.1"
/db_xref="GI:18585770"
/db_xref="InterimID:146438"
CDS join(383374..383520,384849..385088)
    /gene="LOC146438"
    /note="Located on Accession NT_015360"
    /codon_start=1
    /protein_id="XP_085464.1"
    /db_xref="GI:18585771"
    /db_xref="InterimID:146438"
variation 384113
    /gene="LOC146438"
    /note="WARNING: map location ambiguous"
    /allele="G"
    /allele="C"
    /db_xref="dbSNP:2741933"
CDS 385014..385088
    /gene="LOC146438"
    /note="Located on Accession NT_015360"
    /codon_start=1
    /protein_id="XP_036491.1"
    /db_xref="GI:14777843"
    /db_xref="InterimID:146438"
gene 386361..394632
    /gene="LOC124212"
    /note="Located on Accession NT_015360"
    /db_xref="InterimID:124212"
mRNA join(386361..386409,389194..389324,394330..394388,
    394524..394632)
    /gene="LOC124212"
    /product="hypothetical gene LOC124212"
    /note="Derived by automated computational analysis using
    gene prediction method: GenomeScan."
    /transcript_id="XM_064032.1"
    /db_xref="GI:17487928"
    /db_xref="InterimID:124212"
CDS join(386361..386409,389194..389324,394330..394388,
    394524..394632)
    /gene="LOC124212"
    /note="Located on Accession NT_015360"
    /codon_start=1
    /protein_id="XP_064032.1"
    /db_xref="GI:17487929"
    /db_xref="InterimID:124212"
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    /allele="T"
    /allele="C"
    /db_xref="dbSNP:2294149"
variation 392402
    /gene="LOC124212"
    /allele="T"
    /allele="C"
    /db_xref="dbSNP:2741932"
variation 392608
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variation      393575
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variation      394912
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variation      396036
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variation      396292
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                /db_xref="dbSNP:909406"
variation      396819
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                /db_xref="dbSNP:909405"
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variation      399526
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variation      399783
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variation      400027
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                /db_xref="dbSNP:2056891"
variation      401344
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                /allele="G"
                /db_xref="dbSNP:2017820"
gene           402953..406919
                /gene="FLJ14549"
                /note="Located on Accession NT_015360"
                /db_xref="LocusID:84891"
mRNA           join(402953..403271,403497..403764,403985..404049,
                404216..404273,405167..406919)
                /gene="FLJ14549"
                /product="hypothetical protein FLJ14549"
                /note="unclassified transcription discrepancy; Derived by
                automated computational analysis using gene prediction

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method: BLAST. Supporting evidence includes similarity to:
2 mRNAs"
/transcript_id="NM_032805.1"
/db_xref="GI:14249487"
/db_xref="LocusID:84891"
CDS      join(403041..403271,403497..403764,403985..404049,
404216..404273,405167..406722)
/gene="FLJ14549"
/codon_start=1
/evidence=not_experimental
/product="hypothetical protein FLJ14549"
/protein_id="NP_116194.1"
/db_xref="GI:14249488"
/db_xref="LocusID:84891"
STS      406715..406851
/gene="FLJ14549"
/standard_name="RH91869"
/db_xref="UniSTS:89322"
variation 409291
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/db_xref="dbSNP:909404"
variation 410679
/allele="T"
/allele="C"
/db_xref="dbSNP:2092016"
variation 411060
/allele="T"
/allele="C"
/db_xref="dbSNP:2092015"
variation 412296
/allele="T"
/allele="C"
/db_xref="dbSNP:2360173"
STS      413634..413814
/standard_name="STS-M59807"
/note="WARNING: map location ambiguous"
/db_xref="UniSTS:12359"
variation 413787
/note="WARNING: map location ambiguous"
/allele="T"
/allele="G"
/db_xref="dbSNP:2472684"
gene      complement(413853..420635)
/gene="LOC124213"
/note="Located on Accession NT_015360"
/db_xref="InterimID:124213"
mRNA      complement(join(413853..414179,420474..420635))
/gene="LOC124213"
/product="similar to natural killer cell transcript 4"
/note="Derived by automated computational analysis using
gene prediction method: GenomeScan."
/transcript_id="XM_064033.1"
/db_xref="GI:17487930"
/db_xref="InterimID:124213"
CDS      complement(join(413853..414179,420474..420635))
/gene="LOC124213"
/note="Located on Accession NT_015360"
/codon_start=1
/protein_id="XP_064033.1"

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/db_xref="dbSNP:2741929"
variation 413918
/note="WARNING: map location ambiguous"
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/db_xref="dbSNP:2741928"
variation 414247
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/db_xref="dbSNP:2741927"
variation 414354
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variation 417873
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variation 418365
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/db_xref="dbSNP:2005948"
variation 418959
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/db_xref="dbSNP:2360171"
variation 419114
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variation 419122
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variation 420260
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variation 420890
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variation 421102
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422251
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variation /db_xref="dbSNP:2015620"
422399
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422473
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variation /db_xref="dbSNP:2717688"
422508
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variation /db_xref="dbSNP:2717689"
422545
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422812
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422989
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423167
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variation /db_xref="dbSNP:2257551"
423407
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variation /db_xref="dbSNP:2717671"
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423715
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variation /db_xref="dbSNP:2717670"
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              /db_xref="dbSNP:2717669"
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              /allele="G"
              /allele="C"
              /db_xref="dbSNP:2741925"
variation    423797
              /allele="T"
              /allele="C"
              /db_xref="dbSNP:2015174"
variation    423810
              /allele="G"
              /allele="A"
              /db_xref="dbSNP:2717677"
variation    425966
              /allele="T"
              /allele="C"
              /db_xref="dbSNP:1810409"
gene          complement(426262..430150)
              /gene="NK4"
              /note="Located on Accession NT_015360"
              /db_xref="LocusID:9235"
              /db_xref="MIM:606001"
mRNA          complement(join(426262..426822,427573..427632,
              427802..427828,428199..428435,429988..430030,
              430127..430150))
              /gene="NK4"
              /product="natural killer cell transcript 4"
              /note="unclassified transcription discrepancy; Derived by
              automated computational analysis using gene prediction
              method: BLAST. Supporting evidence includes similarity to:
              1 mRNA"
              /transcript_id="NM_004221.1"
              /db_xref="GI:4758811"
              /db_xref="LocusID:9235"
              /db_xref="MIM:606001"
STS          426276..426456
              /standard_name="STS-M59807"
              /note="WARNING: map location ambiguous"
              /db_xref="UniSTS:12359"
variation    426429
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              /allele="T"
              /allele="G"
              /db_xref="dbSNP:2472684"
CDS          complement(join(426457..426822,427573..427632,
              427802..427828,428199..428435,429988..430002))
              /gene="NK4"
              /note="unclassified translation discrepancy"
              /codon_start=1
              /product="natural killer cell transcript 4"
              /protein_id="NP_004212.2"
              /db_xref="GI:11072104"
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              /db_xref="MIM:606001"
variation    426509
              /note="WARNING: map location ambiguous"

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/db_xref="dbSNP:2239302"
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/db_xref="UniSTS:33443"
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variation 428694
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variation 428697
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variation 428734
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                /db_xref="dbSNP:1534864"
STS            435116..435277
                /standard_name="SHGC-61127"
                /db_xref="UniSTS:16544"
variation      435293
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variation      437651
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gene           complement(438492..448263)
                /gene="MMPL1"
                /note="synonym: MMP20; Located on Accession NT_015360"
                /db_xref="LocusID:4328"
mRNA           complement(join(438492..439979,445263..445555,
                445665..445800,448247..448263))
                /gene="MMPL1"
                /product="matrix metalloproteinase-like 1"
                /note="Derived by automated computational analysis using
                gene prediction method: BLAST. Supporting evidence
                includes similarity to: 1 mRNA"
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                /db_xref="LocusID:4328"
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                /db_xref="dbSNP:1064948"
STS            438862..439008
                /standard_name="SGC32543"
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variation      438921
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variation      439146
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                /db_xref="dbSNP:741942"
CDS            complement(join(439861..439979,445263..445555,
                445665..445800,448247..448250))
                /gene="MMPL1"
                /note="matrix metalloproteinase 20"
                /codon_start=1
                /product="matrix metalloproteinase-like 1"
                /protein_id="NP_004133.1"
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variation 443040
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variation 443155
/note="WARNING: map location ambiguous"
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variation 443348
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variation 443381
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variation 443603
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variation 443785
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variation 443848
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variation 443992
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variation 448721
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variation 451534
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/db_xref="dbSNP:1004792"

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/db_xref="UniSTS:148327"

STS 451762..451924
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/db_xref="UniSTS:24815"

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variation 455279
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variation 457566
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variation 461669
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variation 463114
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/db_xref="dbSNP:2878533"
variation 463888
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/db_xref="dbSNP:1972513"
variation 464377
/note="WARNING: map location ambiguous"
/allele="A"
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variation /db_xref="dbSNP:2526261"
465388
/note="WARNING: map location ambiguous"
/allele="C"
/allele="T"
gene /db_xref="dbSNP:1859376"
466644..472860
/gene="LOC146439"
/note="Located on Accession NT_015360"
/db_xref="InterimID:146439"
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472751..472860)
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/product="LOC146439"
/note="Derived by automated computational analysis using
gene prediction method: BLAST."
/transcript_id="XM_085463.1"
/db_xref="GI:18585772"
/db_xref="InterimID:146439"
variation 468486
/gene="LOC146439"
/allele="C"
/allele="G"
variation /db_xref="dbSNP:732261"
468827
/gene="LOC146439"
/allele="A"
/allele="G"
variation /db_xref="dbSNP:2428675"
469454
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469508
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469589
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469955
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471086
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variation /db_xref="dbSNP:2526279"
471225
/gene="LOC146439"
/allele="C"
/allele="T"
variation /db_xref="dbSNP:2717712"
471237

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variation    /gene="LOC146439"
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             /db_xref="dbSNP:2717713"
             471407
             /gene="LOC146439"
             /allele="C"
             /allele="T"
             /db_xref="dbSNP:2526280"
CDS          join(472432..472628,472751..472838)
             /gene="LOC146439"
             /note="Located on Accession NT_015360"
             /codon_start=1
             /protein_id="XP_085463.1"
             /db_xref="GI:18585773"
             /db_xref="InterimID:146439"
variation    473879
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             /db_xref="dbSNP:2244494"
variation    474552
             /allele="C"
             /allele="G"
             /db_xref="dbSNP:2011561"
variation    475017
             /allele="A"
             /allele="C"
             /db_xref="dbSNP:2079244"
variation    475694
             /allele="C"
             /allele="G"
             /db_xref="dbSNP:1052458"
gene         complement(475811..479518)
             /gene="MGC2655"
             /note="Located on Accession NT_015360"
             /db_xref="LocusID:79228"
mRNA         complement(join(475811..475982,476059..476193,
             476279..476389,476486..476548,476643..476692,
             476778..476880,476972..477043,477146..477194,
             477271..477308,477393..477496,477571..477635,
             477736..477847,479194..479366,479473..479518))
             /gene="MGC2655"
             /product="hypothetical protein MGC2655"
             /note="unclassified transcription discrepancy; Derived by
             automated computational analysis using gene prediction
             method: BLAST. Supporting evidence includes similarity to:
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             /transcript_id="NM_024339.1"
             /db_xref="GI:13236588"
             /db_xref="LocusID:79228"
CDS          complement(join(475902..475982,476059..476193,
             476279..476389,476486..476548,476643..476692,
             476778..476880,476972..477043,477146..477194,
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             477736..477818))
             /gene="MGC2655"
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variation      /db_xref="dbSNP:2717664"
                477927
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gene           /db_xref="dbSNP:2526260"
                479612..480927
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                /note="Located on Accession NT_015360"
mRNA           /db_xref="LocusID:54985"
                join(479612..479712,480029..480085,480198..480326,
                480561..480927)
                /gene="FLJ20568"
                /product="hypothetical protein FLJ20568"
                /note="unclassified transcription discrepancy; Derived by
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                method: BLAST. Supporting evidence includes similarity to:
                1 mRNA"
                /transcript_id="NM_017885.1"
                /db_xref="GI:8923535"
                /db_xref="LocusID:54985"
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                480561..480696)
                /gene="FLJ20568"
                /codon_start=1
                /evidence=not_experimental
                /product="hypothetical protein FLJ20568"
                /protein_id="NP_060355.1"
                /db_xref="GI:8923536"
                /db_xref="LocusID:54985"
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                /allele="A"
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variation      /db_xref="dbSNP:2285974"
                480781
                /gene="FLJ20568"
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                /db_xref="dbSNP:11042"
STS           480791..480911
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                /standard_name="RH41886"
                /db_xref="UniSTS:25755"
variation      480853
                /gene="FLJ20568"
                /allele="C"
                /allele="T"
                /db_xref="dbSNP:1050104"

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gene      complement(481179..483199)
          /gene="FN14"
          /note="Located on Accession NT_015360"
          /db_xref="LocusID:51330"
          /db_xref="MIM:605914"
mRNA      complement(join(481179..481788,481870..482004,
          482240..482344,483067..483199))
          /gene="FN14"
          /product="type I transmembrane protein Fn14"
          /note="Derived by automated computational analysis using
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          includes similarity to: 3 mRNAs"
          /transcript_id="XM_036570.1"
          /db_xref="GI:14777984"
          /db_xref="LocusID:51330"
          /db_xref="MIM:605914"
STS       481211..481290
          /standard_name="STS-T56712"
          /db_xref="UniSTS:33040"
variation 481433
          /allele="T"
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          /db_xref="dbSNP:1044326"
variation 481596
          /allele="A"
          /allele="G"
          /db_xref="dbSNP:13209"
CDS       complement(join(481733..481788,481870..482004,
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          /note="Located on Accession NT_015360"
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          /db_xref="GI:14777985"
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                /db_xref="dbSNP:2717704"
gene           485386..488845
                /gene="CLDN6"
                /note="Located on Accession NT_015360"
                /db_xref="LocusID:9074"
mRNA           join(485386..485410,487516..488845)
                /gene="CLDN6"
                /product="claudin 6"
                /note="Derived by automated computational analysis using
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                /transcript_id="XM_012518.3"
                /db_xref="GI:17487954"
                /db_xref="LocusID:9074"
variation      485972
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variation      487391
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CDS            487537..488199
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                /note="Located on Accession NT_015360"
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                /protein_id="XP_012518.1"
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variation      487963
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                /allele="A"
                /allele="G"
                /db_xref="dbSNP:2257295"
variation      488861
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                /allele="A"
                /db_xref="dbSNP:2717700"
gene           complement(489542..490195)
                /gene="CLDN9"
                /note="Located on Accession NT_015360"
                /db_xref="LocusID:9080"
mRNA           complement(489542..490195)
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                /product="claudin 9"
                /note="Derived by automated computational analysis using
                gene prediction method: BLAST. Supporting evidence
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                /transcript_id="NM_020982.1"
                /db_xref="GI:11141860"
                /db_xref="LocusID:9080"

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CDS complement(489542..490195)
/gene="CLDN9"
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/product="claudin 9"
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/db_xref="GI:11141861"
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variation 490410
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/db_xref="dbSNP:2231608"

variation 490414
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variation 490911
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/db_xref="dbSNP:2231606"

variation 491006
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variation 491887
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variation 491956
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variation 492936
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variation 493019
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variation 495678
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variation 495940
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/db_xref="dbSNP:2526268"

STS 496210..496336
/standard_name="SHGC-60552"
/db_xref="UniSTS:74889"

STS 496216..496396
/standard_name="RH69739"

STS	/db_xref="UniSTS:81551" 496299..496429 /standard_name="SHGC-61135" /db_xref="UniSTS:56330"
variation	496999 /allele="C" /allele="T" /db_xref="dbSNP:2526270"
variation	497100 /allele="T" /allele="A" /db_xref="dbSNP:2717706"
variation	498102 /allele="C" /allele="G" /db_xref="dbSNP:2717674"
variation	498734 /allele="A" /allele="G" /db_xref="dbSNP:1635257"
variation	498736 /allele="A" /allele="G" /db_xref="dbSNP:1635258"
variation	498750 /allele="G" /allele="T" /db_xref="dbSNP:1635259"
variation	498754 /allele="A" /allele="G" /db_xref="dbSNP:1635260"
variation	498772 /allele="G" /allele="A" /db_xref="dbSNP:1236079"
variation	498800 /allele="T" /allele="C" /db_xref="dbSNP:1236078"
variation	498840 /allele="C" /allele="A" /db_xref="dbSNP:1236077"
variation	498852 /allele="G" /allele="C" /db_xref="dbSNP:1236076"
variation	498900 /allele="G" /allele="A" /db_xref="dbSNP:1236075"
variation	498908 /allele="C" /allele="A" /db_xref="dbSNP:1236074"
variation	498934 /allele="G" /allele="A" /db_xref="dbSNP:1236073"

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variation      500803
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variation      500983
                /allele="A"
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                /db_xref="dbSNP:2526273"
gene            complement(501553..502260)
                /gene="LOC146440"
                /note="Located on Accession NT_015360"
                /db_xref="InterimID:146440"
mRNA            complement(join(501553..501999,502226..502260))
                /gene="LOC146440"
                /product="LOC146440"
                /note="Derived by automated computational analysis using
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                /transcript_id="XM_085470.1"
                /db_xref="GI:18585774"
                /db_xref="InterimID:146440"
STS            501598..501680
                /standard_name="RH92900"
                /db_xref="UniSTS:85787"
CDS            complement(join(501712..501999,502226..502252))
                /gene="LOC146440"
                /note="Located on Accession NT_015360"
                /codon_start=1
                /protein_id="XP_085470.1"
                /db_xref="GI:18585775"
                /db_xref="InterimID:146440"
variation      502203
                /allele="C"
                /allele="T"
                /db_xref="dbSNP:2256045"
variation      502282
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variation      502438

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              /db_xref="dbSNP:2526274"
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              /db_xref="dbSNP:886429"
variation    516916
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              /db_xref="dbSNP:886428"
variation    518275
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              /db_xref="dbSNP:2005712"
variation    518782
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              /db_xref="dbSNP:2335826"
gene         523712..530768
              /gene="PKMYT1"
              /note="synonym: MYT1; Located on Accession NT_015360"
              /db_xref="LocusID:9088"
              /db_xref="MIM:602474"
mRNA        join(523712..523913,526530..526897,527749..528242,
              528905..529011,529144..529316,529404..529561,
              530346..530423,530497..530768)
              /gene="PKMYT1"
              /product="membrane-associated tyrosine- and
              threonine-specific cdc2-inhibitory kinase"
              /note="unclassified transcription discrepancy; Derived by
              automated computational analysis using gene prediction

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1 mRNA

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/db_xref="LocusID:9088"

/db_xref="MIM:602474"

CDS join(523904..523913,526530..526897,527749..528242,528905..529011,529144..529316,529404..529561,530346..530423,530497..530608)

/gene="PKMYT1"

/note="dual-specificity kinase phosphorylates Cdc2 on both Thr14 and Tyr15"

/codon_start=1

/product="membrane-associated tyrosine- and threonine-specific cdc2-inhibitory kinase"

/protein_id="NP_004194.1"

/db_xref="GI:4758928"

/db_xref="LocusID:9088"

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variation 529374

/gene="PKMYT1"

/allele="G"

/allele="A"

/db_xref="dbSNP:2074528"

variation 529957

/gene="PKMYT1"

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/allele="C"

/db_xref="dbSNP:886427"

gene complement(530079..534194)

/gene="LOC124222"

/note="Located on Accession NT_015360"

/db_xref="InterimID:124222"

mRNA complement(join(530079..532046,532183..532404,533721..534194))

/gene="LOC124222"

/product="similar to RIKEN cDNA 1500004C10"

/note="Derived by automated computational analysis using gene prediction method: BLAST. Supporting evidence includes similarity to: 1 mRNA"

/transcript_id="XM_058784.2"

/db_xref="GI:18585776"

/db_xref="InterimID:124222"

CDS complement(join(531613..532046,532183..532404,533721..533886))

/gene="LOC124222"

/note="Located on Accession NT_015360"

/codon_start=1

/protein_id="XP_058784.1"

/db_xref="GI:17487953"

/db_xref="InterimID:124222"

variation 534927

/allele="T"

/allele="C"

/db_xref="dbSNP:2285829"

gene complement(535182..539152)

/gene="MGC10791"

/note="Located on Accession NT_015360"

/db_xref="LocusID:79412"

mRNA complement(join(535182..535751,536116..536245,

536322..536651,536766..536919,537112..537236,
537330..537421,538528..538702,538947..539152))
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/product="hypothetical protein MGC10791"
/note="Derived by automated computational analysis using
gene prediction method: BLAST. Supporting evidence
includes similarity to: 1 mRNA"
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/db_xref="GI:14777965"
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variation 535980
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/db_xref="dbSNP:2285828"
CDS complement(join(536223..536245,536322..536651,
536766..536919,537112..537236,537330..537421,
538528..538702,538947..539040))
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/note="Located on Accession NT_015360"
/codon_start=1
/protein_id="XP_036566.1"
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Date: December 20, 2005
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Inventor: Ting et al

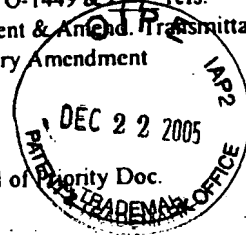
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- ☐ Declaration & POA
- ☐ Assignment and Fee
- ☐ Small Entity Statement
- ☐ Formal Drawings/ sheets
- ☐ Associate Power of Attorney
- ☐ Exp. Mail ☒ 1st Class Mail

☒ Other: return postcard

- ☐ Check \$
- ☒ IDS & PTO-1449 & 119 refs.
- ☐ Amendment & Amend. Transmittal
- ☐ Preliminary Amendment
- ☐ Issue Fee
- ☐ Brief
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- ☐ Submittal of Priority Doc.



Respectfully submitted,
MYERS BIGEL SIBLEY & SAJOVEC, P.A.
Attorneys for Applicant